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AY065153 Arabidops
AC008075 Arabidops
AP004030 Oryza sat
AP004536 Lotus jap
AP004575 Oryza sat
AC006917 Genomic s
AB015477 Arabidops
AJ271639 Elaels gu
AF327424 Arabidops
AC016041 Genomic s
AC016041 Genomic s
AC016041 Genomic s
AC07659 Arabidops
AC002354 Arabidops
AC07559 Arabidops
AC07659 Arabidops
AC07660 Oryza sat
AC06460 Oryza sat
AC06460 Oryza sat
AC06400 Oryza sat
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                                                                                                                                                                                                                                                                        AP003134 Staphyloc
AP003363 Staphyloc
AP00369 Oryza sat
AC06582 Homosapi
AC095340 Rattus no
AC07985 Oryza sat
AC067971 Sequence
U78866 Arabidopsis
AB025621 Arabidops
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0 Homo sapi
A06730234FM
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AC092671 Homo sapi
AC098859 Homo sapi
AC068493 Mus muscu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lycopersicon pennellii.
Lycopersicon pennellii
Eukaryota: Viridiplantaes Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                           Arabidops
Arabidops
Arabidops
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                       Lycopers1
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Homo sapi
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Unpublished
2 (bases i to 811)
Frary,A., Nesbitt,T.Clint., Frary,A., Grandillo,S., van der
Knaap,E., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 811)
Frary, A., Nesbitt, T.Clint., Frary, A., Grandillo, S., van der Knaap, E., Cong, B., Liu, J., Meller, J., Elber, R., Alpert, K.B. Tanksley, S.D.
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AF261775
AF261775.1 GI:8272627
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AB026658
EGU271639
AF327424
AC016041
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AC022354
AC007659
AY054680
ATU78870
OSJN00003
  AF261775
AF261774
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AF411806
AX072397
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60.7 2821

25.1 61382

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11.5 1146017

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11.6 88989

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11.7 86014

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11.2 119091

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                                                                     July 15, 2002, 06:36:27; Search time 1826.14 Seconds (without alignments) 5538.043 Million cell updates/sec
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Copyright (c) 1993 - 2000
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                                                   nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                         Gaps
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Tanksley,S.D.
Direct Submission
Submitted (28-APR-2000) Plant Breeding, Cornell University,
Emerson Hall, Ithaca, NY 14653, USA
Location/Qualifiers
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Pred. No. 7.5e-71;
0; Mismatches 0;
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ilarity 80.4%;
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
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1 (bases 1 to 821)
Frary,A., Grandillo,S., van der
Frary,A., Cong,B., Liu,J., Meller,J., Elber,R., Alpert,K.B.
Tanksley,S.D.

fw2.2: a quantitative trait locus key to the evolution of ton
                                                                                                                                                                                                                                                                                                                                                     Submitted (28-ARR-2000) Plant Breeding, Cornell University, Emerson Hall, Ithaca, NY 14853, USA Location/Qualifiers 1. .821
                                                                                                                                                                                                                                                                                   Frary, A., Nesbitt, T.Clint., Frary, A., Grandillo, S., van der
Knaap, E., Cong, B., Liu, J., Meller, J., Elber, R., Alpert, K.B.
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Lycopersicon esculentum ORFX (ORFX) gene, complete cds
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larity 79.4%; Pred. No. 1.4e-68;
Conservative 0; Mismatches 6;
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/gene≕"ORFX"
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Direct Submission
Submitted (28-APR-
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Unpublished
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Qy 209 Db 356	9catgtgggagtagaggtgcattatattgtttgctgggactgacaggattgc 259 	209
Oy 260 Db 416	O ctagcctatattcctgcttctacaggtctaaaatgaggggcaatatgatctggaagagg 319 	
Oy 320 Db 476	O caccttgtgttgattgtctgtacatgtattctgtgaaccttgtgctctttgccaagaat 379 	18819
Oy 380 Db 536	O acagagagcttaagaaccgtggctttgatatgggaatagg 419 	Db 18759 CACCTTGTC Qy 380 acagagagc
RESULT 3 AF411809/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS	3 /c AF411809 127892 bp DNA linear PLN 07-OCT-2001 DN Lycopersicon esculentum BAC clone FW2.2, complete sequence. N AF411809 AF411809.1 GI:15987774	RESULT 4 AF411806 LOCUS AF41180 DEFINITION LYCOPERACESSION AF41180
SOURCE ORGANISM		SISM
REFERENCE AUTHORS TITLE	E 1 (bases 1 to 127892) S van der Hoeven, R.S. and Tanksley, S.D. Deductions about the number, organization and evolution of genes in the tomato genome based on analysis of large EST collection and selective genomic sequencing	REFERENCE 1 (bas AUTHORS van der TILE Deductit
JOURNAL REFERENCE AUTHORS TITLE JOURNAL		selecti JOURNAL Unpubli REFERENCE 2 (bas AUTHORS van der TITLE Direct JOURNAL Submitt
BASE COUNT	co	FEATURES SOURCE
ORIGIN Query Match Best Local	tch 60.7%; Score 298.4; DB 8; Length 127892; al Similarity 79.4%; Pred. No. 7.2e-69;	BASE COUNT 20121 ORIGIN
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Oy 61 Db 19119	61 tatgtatctgcccccggcaccaccacggcgcggtggtcaactggtctttgtcactgttt 120 	Db 21362 CATGTGCTY Qy 268 tattcctg
Qy 121 Db 19059	1 gatgacctgctaactgtttagttactagtgtttgccttgtatcacctttggacagatt 180 	Db 21422 TATTCCTAG Qy 328 gttgattgi
Qy 181 Db 18999	1 tctgaaatactaaacaaaggaacaactt	Db 21482 GCGGATTGI Qy 387 gcttaagae
Qy 209 Db 18939	9 208 9 GGATAAATTCAATTTATTTGATATTTGGTTACCAAGAATATGATGTTTGTGTTTGTT	Db 21542 GCTTAAGA

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dases 1 to 61382) er deven, R.S. and Tanksley, S.D. er Hoeven, R.S. and Tanksley, S.D. tions about the number, organization and evolution of genes in comato genome based on analysis of large EST collection and tive genomic sequencing
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                                                               Jases 1 to 61382)
ler Hoeven, R. S. and Tanksley, S. D.
It Submission
tted (20-MG-2001) Plant Breeding, Cornell University, 252
on Hall, Ithaca, NY 14850, USA
Location/Qualifiers
1. 61382
-catgigggagtagaggtgcattatattgtttgctgggactgacaggattgc 259
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                                                                                                                                                                                                       /organism="Lycopersicon esculentum"
/db_xref="taxon:4081"
/clone="Clenson_ID 207 BAC"
/note="fragment 2"
a 11562 c 10377 g 19322 t
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5;

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

TITLE

DEFINITION

RESULT AY072397

ACCESSION

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Arabidopsis thaliana unknown protein (At3g18480; MYF24.19) mRNA, complete cds.
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Litary
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Submitted (03-DEC-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagagctt 390
                                                                                                                                                                                                                                                                                                                            271 tcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcaccttgtgtt 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 GATTGCCTTAAACATTTCTGCTGTGAGCTTTGTTCTTTGACCCAACAATACCGTGAACTC 409
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                                                                                                                                                                                                             154 tgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt
                                                                                                                                                              170 TGTCCATGTATCACCTITGGCCAAGTCGCCGAGATTGTAGATCGAGGATCCACATGGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                391 aagaaccgtggctttgatatgggaatagggtggcaagctaataggatagacaa 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             410 AAGCACCGCGGTTACGATATGAGTCTTGGATGGGCGGGGAACGTGGAGAGACAA 463
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/note="This clone is in pBluescript
ecotype: Columbia"
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/db_xref="taxon:3702"
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AY065153.1 GI:17473787
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Spermatophyta; Magnollophyta; endicotyledons; core endicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases I to 683)

S Nguyen,M., Karlin-Neumann,G., Southwick,A., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Carninci,P., Chen,H., Cheuk,R., Chung,M.K., Hayashizaki,Y., Ishida,J., Kamiya,A., Kawai,J., Kim,C., Lin,J., Liu,S.X., Narusaka,M., Pham,P.K., Sakano,H., Sakano,H., Sakunai,T., Satou,M., Seki,M., Shinn,P., Yamada,K., Shinnzaki,K., Ecker,J., Theologis,A. and Davis,R.W.
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CELCSLTQQYRELKHRGYDMSLGWAGNVERQONQGGVAMGAPVFQGGMTR"
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                                                                        AY072397 683 bp mRNA linear PLN 21-JAN-:
Arabidopsis thaliana unknown protein (At1g14870) mRNA, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e-mail for correspondence: arab@sequence.stanford.edu
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ecotype: Columbia"
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/clone="RAFL09-28-D02"
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FLI_CDNA.
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BASE COUNT ORIGIN

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FEATURES

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I (bases 1 to 98942)

I (bases 1 to 98942)

S Vysotskala,V.S., Schwartz,J.R., Yu,G., Toriumi,M., Lenz,C., Liu,S., Lee,J.M., Li,J., Gonzalez,A., Liu,A., Liu,K., Vaysberg,M., Sakano,H., Chin,C., Chiou,Y., Altafi,H., Araujo,R., Brooks,S., Buehler,E., Chao,Q., Conn,L., Conway,A.B., Dunn,P., Hansen,N., Howng,B., Hulzar,L., Khan,S., Kim,C., Palm,C., Rowley,D., Shinn,P., Walker,M., Davis,R.W., Ecker,J.R., Federspiel,N.A. and Theologis.A.
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152 q 225 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-JUL-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA 3 (bases 1 to 98942)
                                                                                                                                                                                                                                                                                                                                90 gcggtggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactag 149
                                                                                                                                                                                                                                                                                                                                                                   133 GCAATGGACTTCTGGTCTTTTCAGCTGCATGGAAGACAGTGAAACTGCTTGCCTCACATG 192
                                                                                                                                                                                                                                                                                                                                                                                                               tgtttgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttc 209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 GTTCTCATGCACTTACCGGACCAAGATCCGAAGCAAATTCGGGTTACCGGAGTCTCCAAC 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      373 TTCGGATTGCGTCACTCATTTTTTTGTGAATGTTGTGCTTTTGCCAAGAACACCGTGA 432
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                                                                                                                                                                                                                                                    Score 106.2; DB 8;
Pred. No. 1.2e-17;
0; Mismatches 143;
              /gene="At3g18480; MYF24.19"
                                     /codon_start=1
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                                                                                                                                                                                                                                                  Query Match 21.6%;
Best Local Similarity 58.4%;
Matches 205; Conservative (
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.4358,
.6282)
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RRVSNSLKKFTGKPLPLTCTPWKFGSWMGGDRDGNPVTAKVSLLIFYDLNSKPTGHE
RISLLSRWMAIDLYIREVDSLRFELSTDRCSDRFSRLADKILEKDYMPPNLOKQNEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDVLAVELLØKDARLALTSEHGKPCPGGTLRVVPLFETVNDLRAAGPSIRKLLSIDWY
REPLOKNHANGHGEWMGTSDSGKDAGRFTAAMELYKAQDEWYAACNEFGTKITLEHGR
GGSIGRGGPTYLAJOSQPPGSYNGSIRSTEGGEWYQAKFGIPQTARQLEYYTAYL
LATLKPPQPPREEKWRNLMEEISGISCQHYRSTVYENPEFLSYFHEATPQAELGFLNI
GSRPFRKRKSSSGIGHLAAIPWYFAWTOTRFVLPAMLGYGGLKGYSEKGHADDLKEMY
KEWPFFGSTLELIEWARADIPWTKHYDEQLYSEKRRGLGTELKEMY
GEWPFFGSTLELIEWARADIPWTKHYDEQLYSEKRRGLGTELKELWTTEKYVLVI
SGHEKLLQDNKSLKKLIDSRLPYLNAMMLQYEILKRILRRDEDNNKLRRAALTINGTING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MIDTIDDIAEEISFQSFEDDCKLLGSLFHDVLQREVGNPFMEKV
ERIRILAQSALNLRWAGIEDTANLLEKQLTSEISKMPLEEALTLARTFTHSLNLMGIA
DTHHSQLLQSGISPDELYKTVCKQEVEIVLTAHPTQINRRTLQYKHIRIAHLLEYNTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSESDWEKIDNGSRSGLTSRGSFSSTSOLLLORKLFEESQVGKTSFOKLLEPPERKRA
GSAPYRIVLGEVKELVYRRILELLIJEGLPCEYDPRNSYETSDOLLEPLLLCYESLO
SSGAPYLADGERLADITRNSTREGLELJIEGLPCEADHRNSYETSDOLLEPLLLCYSEND
SSGAPYLADGERLADITRNSTREGMIJWLIDLRQEAARHSEALDAITYLDMGTYSEWD
EEKKLEFLTRELKGKRPLVPQCIKVGPDVKEVLDTRYVAAELGSESLGAYVISAASNA
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TETSLIKTVKSSLGRLSIFGNKGREQSRVIQVLKINLSLCDFYLSTIHGFVVLMVLML
FKQVHKKLASSGSNNDVYETELLEKIADDTDAAKEFFACLDMQLNKVNOFYKTKEKEF
LERGECLKKQMDILIELKDAFKQKQANGESTQESKEDDSISCTISCEYDSVRGRTEEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLQVSCLDNLEDNGEEALESIGSEEPTKANNEDSKLTTVSSRVFSCOCKNVKTKIPLT
NPSRTFSAISYLINGSSSKKNGPDGGNKLQISKKKLSHAEKMIKGALTELFKGLNYLK
TYRNLNILAFMNILKKFDKVSIKSEOFKQSFYKVFFSIFDFKTSPFIFQVTGKQILPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLFTGCFVALLAGYIIVAHLTGMYRQHSANTFYMETAYPVLRRKLMANFHVFCSMFGL
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MLDFFMADQLCSQVPMLRNLEYIACYYITGSYATQDYEYCMRVKYYRDLAYAVSFLPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YLKVVESSYFNISDKVMILSDEVEEWFIKHLAGENRRKAMKYLKPHHRKESHSVTFFI
                                                                                                                                                                                   Submitted (17-AUG-1999) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA on Aug 10, 1999 this sequence version replaced gi:5525042. The sequence of BAC F2415 from Arabidopsis thaliana chromosome 1. Location/Qualifiers
    Gene Expression Center, 800 Buchanan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12650. .16489
/gene="F24J5.2"
join(12650. .13268,13470. .14071,14223. .14352,14653. .1
14855. .15136,15232. .15381,15502. .18654,15754. .16032,
/gene="F24J5.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    jóin(1121. 1276,1432. 1595,1764. 1821,1940. 2017,
2103. 2171,2251. 2329,2407. 2483,2575. 2713,2899.
3364. 3386,3492. 3728,3827. 3952,4035. 4136,4212.
4459. 4557,4638. 4726,4847. 4973,5048. 5254,5458.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Similar to gb|X90982 phosphoenolpyruvate carboxylase (ppcl) from Solanum tuberosum." /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                           1. .98942
/organism="Arabidopsis thaliana"
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/protein_id="AAD49969.1"
/db_xref="G1:5734704"
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/protein_id="AAD49968.1"
/db_xref="G1:5734703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3702"
Submitted (10-AUG-1999) Plant
                                Street, Albany, CA 94710, USA 4 (bases 1 to 98942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="F24J5"
1121. .6282
/gene="F24J5.1"
                                                                                                              Theologis, A.
Direct Submission
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a member of PF 00122 E1-E2 ATPases family."
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58.5%;
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Best Local Similarity 58.5
Matches 227; Conservative
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                                                                                                              join(18096. .18247,18359. .18485,18566. .18694,18799. .18903)
/gene="F24J5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEHCGRRKKSSELESESRRGSKLVTGEYIGKSYRGDEEREVRPRRKKSSSCSSYYSLA
SSGEEESDTEDOLEEDVEIYRENVRSEEKKVVDOSARRLKSRKEASOMFRKKNDEST
GVDSRYQKQ IFEGENSWQAVLLUQRRKKKFSQTERVSESTGNYEEDBHSTRKRDESST
GVDSRQKQKIPEREPORVHSITRNDSGNENIESSGHOLKERLETRYSSEDRYSEMRRR
TKYSSSQEEGINVLQNFPEVTNNQQPLVEERISKQAGTRRTTEHISESSEIHDIDIRN
TYYQQREDOIRNQEVHAGLYSCLQSERKQOYHIEHNPLQTTQSDRTSVSYSHTSDAV
RYTEIQRKSERKLIGGGSTAVQSDSRVCKNGAQKEDSRLDHANSKKDGQTLGLGSY
GSKLSEEASSSGOSLAMSSTKLQLVDLVSEENQGSETTLIPPSSQLYSRRSGQSYRTG
GVSIQEISHGTSESSTYARASDSSYSSTA
                                                                                                                                                                                                                                                                                                                               /translation="MANTAAGWSPVLAPIYSPVNTKPINFHESASFYKPPRPFYKQON
PISALHRSKTTRVIEVVTPKQRNRSFSVFGSLADDSKLNPDBESNDSAEVASIDIKLP
PISALGVFFTCNSCGERTKRLINRHAYEKGLVFVQCAGCLKHHKLVDNLGLIVEYDFRE
TSKDLGTDHV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPTTAAPPPTTTTPPVSAAQPPASEVTPPPAVTPTSPPAPKVAPVISPATPPPQPPQ
PSPASAPTVSPPPVSPPPAPTSPPPTASPPPAPSPPAPASPPAPAPVSPPPVQAPS
PISLPPAPAPAPATKHKKHKKHHHHAPAPAPIPPSPPVLTDPQDTAPAPSPNTV
TIOX"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       region. EST gb|W43306 comes from this gene."
/codon_start=1
/revidence=not_experimental
/protein_id="AAD49971.1"
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/db_xxrf="c1:573470x6"
/translation="MRTYTYRSLOWPTRSRNQQDYCSLLPERSESYKLSKAYTSSRCY
CVSSRSSCCCCSTPSSSSFVKPKVLINPGFVLYGVRQSTLIQWPSFQRRLLVGGGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYVGĒFVKKAKHGVINPETEEQRAESNQLKRRDSRRSSGGSGAKGPSDEMWYTDŠAQG
TPHPGATEGNAAVGNAIFKRNGRSLWNVIADIARLRWGSRAGSPDSSAKPAGRSSPNE
SVSSATWFSGREHDGSSDDNTKGDKVLPQEAPSLHQVEVGQTSPRSQSEYPGTTKLKQ
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PAVMEPPVPRPRMVSGSSSLREQVEQQQPLSAKSQEETGSVSADSALIQRKLQRNKQV
IIYQLYWDFVKDWGLLQHNSNNPWLRNQLMLRQKSIYYFSMVLNLVLRLAWLQTVLHS
SFBHYDYRVTGLFLAALEVIRRGQWNFYRFRIYTDTCVDKIQNICRLENEHLNNAGKF
RAVKTVPLPFREVDEED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGCEVYSSCDGIRRKNRSFKLRCLEESDECCGGRSCSDDVEAMISFLSEELIDEERKW
NLVSRVKEKKKVGNVRKVSVEGSNSYGNGRVSQRVKKPEGFGRRKEIKEDVKLNERYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MESNSIIWSLLLASALISSFSVNAQGPAASPVTSTTAPPPTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RSERHEGVVSSPSSTILEGGSVSNRMSSTSGNQIVGVDEEEGGNFEFRLPETALTEVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YNLVEELRDSTAHAEMICIREGSKALRSWRLADTTLYVTLEPCPMCAGAILQARVNTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWGAPNKLLGADGSWIRLFPGGEGNGSEASEKPPPPVHPFHPKWTIRRGVLESECAGT
MOOFFQLRRKKKKKKKNSDPPTPTDHHHHLPKLLNKMHQVLPFFCL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(join(20404. .20665,20744. .20871,21079. .21166,
21232. .24677))
/gene="F24J5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        join(31249. .31653,31751. .33111,33181. .33291,33368. .336
33736. .33824,33936. .34004,34142. .34345,34427. .34552,
34645. .34743,34827. .35018,35097. .35726)
/gene="p?445.6"
/note="Similar to gb|AF067820 ATPase II from Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 deaminase from Chlamydia trachomatis genome gb|AE001357 and contains a PF|00383 cytidine deaminase zinc-binding region. EST gb|W43306 comes from this gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Contains similarity to gi|3329316 cytosine
                                                                                                                                                                                                                         /evidence=not_experimental
/product="F24J5.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /evidence-not_experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="F24J5.4"
complement(19258. .19926)
/gene="F24J5.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(20404. .24677)
/gene="F24J5.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(19258. .19926)
                                                                                                                                                                                                                                                                         /protein_id="AAD49972.1"
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                                                                                                                                                                                                                                                                                                     /db_xref-"GI:5734707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31249. .35726
/gene="F24J5.6"
                                                                               18096. .18903
/gene="F24J5.3"
                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                    gene
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DGVWKRWYLRPDSSSIFFDPKRAPVAAITHFLTAVMLYSYFIPISLYVSIEIVKVLQS
TRIODIHWYYEABARCARAFRSKULBELGOVDTLLSPKTGTTLCNSWEBTKCSVSYAGT
AYGROYTEVBRAMGREKGGPLYPGSDENDIDMEYSKEAITEBSTYKGFNFRDERIMO
NWYTETHADVIQKFFRLLAVCHTVIPEVDEDTEKISYEASPDEAAFVIAARELGFEF
FWRYTISYRELDLYSGKYRPELYVANVLEFNSTRKRMSYTYGEBOKLLLLCKGA
DNWMFERLSKUGREEEETRDHYNEYALAGGATATLILRYFELDEKEYKVFNERISSEAKS
SVSADRESLIEEVTEKIEKDLILLGATAVEDKLQCOMUNDIFIERISSTKEAGGEF
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Petunia x hybrida PGPS/D12 (PGPS/D12) mRNA, complete cds.
AF049928
                                                                                                                                                                                                                  LSIGDIVKVEKNEFFPADLVLLSSSYEDAICYVETMNLDGETNLKVKQGLEVTSSLRD
EFNFKGFEAFVKCEDPNANLYSFVGTMELKGAKYPLSPQQLLLRDSKLRNTDFIFGAV
IFTGHDTKVIQNSTDPPSKRSMIEKKMDKIIYLMFFWVITMAFIGSVIFGVTTRDDLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METAINIGFACSLLRODMKOIIINLETPEIOSLEKTGEKDVIAKAŠKENVLSOIINGK
TOKYSGGMARPALIIOKSLAYALDDIKHIFELELAVSCASVICCRSSPKOKALYTRL
VKSCNGKTTLAIGDGANDVORLOEAJIGOTSGVEGMOAVMSSDIAAPFRSLERLLI
VHGHWCYRRISTMICYFFYKNITFGFTLELYETYTFSSTPAYNDWFLSLYNVFFSSL
                                                                                                         /translation="mvGGGTKRRRRLQLSKLYTLTCAQACFKQDHSQ1GGPGFSRVV
YCNEPDSPEADSRNYSDNYVRTTKYTLATFLPKSLFEQFRRVANFYFLVTGVLAFTPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVIALGVFDQDVSARYCLKFPLLYQEGVQNVLFSWRRILGWMFNGFYSAVIIFFLCKS
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FFITVYGELPSRISTGAYKVFVEALAPSLSYWLITLEVVVATLMPYFIYSALQMSFFP
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                                                                                                                                                                                 APYTASSAIVPLLFVIGATMVKEGVEDWRRQKQDNEVNNRKVKVHRGDGSFDAKEWKT
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Petunia x hybrida

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Petunia.

1 (bases 1 to 782)

Guyon, V.N., Astwood, J.D., Garner, E.C., Dunker, A.K. and Taylor, L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65547 TGGTCGACTGATTTGTGTGAATGTTGGATGGACATAAACTCATGCTGCTTGACTTGTTGG 65488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65427 GGTGTGAGCGGAGCGATGTACATGATCATATTCATGTTGACCGGGTATGGAGGAAGCAGT 65368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctatattcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcacct 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgtt 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gggagtagaggtgcattatat-----tgtttgctgggactgacaggattgcctagc 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 12; Gaps
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6
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0; Mismatches 149;
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/evidence=not_experimental
/protein_id="AAD49973.1"
/db_xref="G1:5734708"
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Pred. No. 8.8
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Query Match
Best Local 3
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DEFINITION
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                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 1
AP004536
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KEYWORDS
SOURCE
                             REFERENCE
                                                          AUTHORS
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                                                                                                                                                                                                 AUTHORS
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                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
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                                                                                                                                                           2 (bases 1 to 782)
Guyon, V., Astwood, J.D. and Taylor, L.P.
Direct Submitssion
Submitted (23-FEB-1998) Genetics and Cell Biology, Washington State University, Science Hall, Pullman, WA 99164-4234, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_i="AAD02554.1"
/db_xref="G1:4105794"
/db_xref="G1:4105794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

    .782
/organism="Petunia x hybrida"
/db.xref="taxon:4102"
/Lissue_type="germinating petunia pollen treated with
kaempferol"

                       Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia Plant Physiol. 123 (2), 699-710 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tgtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacaga 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgtt 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tgcccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      208 GTAGTGAGTGGAACAGTTTACCTATTGGTTTATCTTGTGACGAGTGGGTTCGGGTGTGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ctatattcctgcttctacaggtctaaaatgagggggggaatatgatctggaagaggcacct 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     328 TGCTCTGATCTCTGTACCCATTGTTGTTGCGAGTACTGCGCATTGTGTCTCAGAGTACAGA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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HTG; HTGS_PHASE2.
Oryza sativa (cultivar:Nipponbare) DNA, clone:OJ1124_H01.
Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 95; DB 8; Length 782;
Pred. No. 1.1e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 145; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product-"PGPS/D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PGPS/D12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="PGPS/D12"
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56.6%;
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201; Conservative
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Matches 20
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ORIGIN
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AP004003/c
TITLE
                                                                                                                                          PUBMED
REFERENCE
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Libert Submission.

Submitted (01-AUG-2001) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba. Tbaraki 305-8602, Japan (E-mail:tsasakiémias-afirc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)

Tel:81-298-38-7441, Fax:81-298-38-7468)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the cope correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced * * by the finished sequence as soon as it is available and * the accession number will be preserved.

* This sequence will be replaced * * by the finished sequence as soon as it is available and * the accession number will be preserved.
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chromosome 4, clone:LjT15N19, TM0097b,
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Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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                                         BAC
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
clone:OJ1124_H01
Published Only in Database (2001) In press
2 (bases 1 to 103550)
Sasaki,T., Matsumoto,T. and Yamamoto,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 103550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90.8; DB 2;
Pred. No. 7.3e-14;
0; Mismatches 112;
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21927 c 21786 g 30082
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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ilarity 59.8%;
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/organism="Oryza sativa"
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/db_xref="taxon:4530"
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Sato,S., Kaneko,T., Nakamura,Y., Asamizu,E., Kato,T. and Tabata,S.
Structural Analysis of a Lotus japonicus Genome. I. Sequence
Features and Mapping of Fifty-six TAC clones which cover the 5.4 Mb
Regions of the Genome
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Sasaki,T., Matsumoto,T. and Yamamoto,K.
Saraki,T., Matsumoto,T. and Yamamoto,K.
Submitssion
Submitted (02-MAY-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11485 TGGTTGCGGTTGCTTGTACTCATGCTTCTACCGTTCCAAGTTGAGACGCCCAATACATGTT 11544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                       Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        252 aggattgcctagattcctgcttctacaggtctaaaatgaggggcaatatgatct 311
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Oryza sativa chromosome 6 clone P0528B02, *** SEQUENCING IN
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HTG: HTGS_PHASE2.
Oryza sativa (cultivar:Nipponbare) DNA, clone:P0528B02.
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                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="LjT library"
/note="TM0097b, a part of TAC clone:TM0097"
13546 c 14460 g 24726 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9e-11;
0; Mismatches 93;
                                                                                                                                                                                                                                                                                                                   /organism="Lotus japonicus"
/db_xref="taxon:34305"
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                                                                                                                                                                                                                                                                                                                                                                        /clone="LiT15N19"
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Nakamura, Y.
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(E-mail:tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 132699)
Chao,O., Shinn,P., Dunn,P., Buehler,E., Kahn,S., Kim,C., Walker,M., Williams,S., Altafi,H., Araujo,R., Conn,L., Conway,A.B.,
Gonzalez,A., Hansen,N.F., Huizar,L., Kremenetskala; L. Lenz,C.,
Li,J., Liu,S., Luros,S., Rowley,D., Schwartz,J., Toriumi,M.,
Vysotskala,V., Yu,G., Davis,R.W., Federspiel,N.A., Theologis,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACUUB917 132699 bp DNA linear PLN 28-JUN-2000 Genomic sequence for Arabidopsis thallana BAC F10B6 from chromosome I, complete sequence.
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Ecker, J.R.
Direct Submission
Submitted (2-FEB-1999) Arabidopsis thaliana Genome Center,
Department of Biology, University of Pennsylvania, 38th Street and
Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11757 GGGACCTIGTATGTTTTGCTGGCGACAATAGGCTGCCAATGGCTGTATGCTTGTACCAAA 11698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11697 CGATCCTCAATGCGGGCACAGTACAACTTGCAACAGTCGCCTGCTTGGACTGCTGCGTC 11638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 223 ggtgcattatattgtttgctgggactgacaggattgcctagcctatattcctgcttctac 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        343 catgtattctgtgaaccttgtgctctttgccaagaatacagagagcttaagaaccgtggc 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  283 aggictaaaaatgaggggggaaatatgaictggaaggaggcacctigitgitgaitgicitgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="P0528B02"
31780 c 31628 g 40874 t
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ASFVSKDESISLGRIFILEANSEEDKCCETLLRKWDOLKPTTOKFVSLVSWVKRIEKEK

CLINNLAKADEVELVSEQNRELDRENKFLRQCSAERSHGSNKFNKRKSIKWMSSP

IEKRIELSSQEFID"

11067. .11306

/note="unknown protein; similar to EST gb|A1995472.1"

/codon_start=1

/evidence=not_experimental
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FLYHQDRESLMEFGNFTDERRAREAESRVRELEEEVRKMSDEIKSRIESFEDCLVDSIL
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PFDLSSFGEGNSRIMSKSGGFNLFVRAYFAFLDRRSILFHDGNRHRYNEESSVLIRLV
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YPEBLHLQCPPLTPKMYIFWLDFLRIRWFDKDVCKSSFTFKOBLVSVGARGALGFNE
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EQSLIVFSEESSFDEMVNNMKSQSELCVILAKIFGSIAVAIAVVGVDYARKVLLPFV
                                                                             VWGHRIYTIYSILFIVFIILIIVTAFITVALTYFQLAAEDHQWWWRSFLCGGSTGLFI
XAYCLYYYXARSDWSGFWQTSFFFGYMACICYGFFLMLGTVGFRAALLFVRHIYRSIK
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KIGKTEADLALKIVAKSMKOGGELKKYFEFCKDLGVSNAQEIPNFVRIPEADVIHLDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTVQRRRKSKFTAEQREAMKDYAAKLGWTLKDKRALREEIRVFCEGIGVTRYHFKTWV
NNNKKFYH"
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complement(join(20071. 20409, 20499. 20573,20648. 20721,
20800. 20887,20957. 211088. 211356,21448. 21906,
22006. 22275,32367. 22570,22840. 22917))
                              GIAGKNSKAEFQAPCRTTKYPREIPPLPWYRSAIPQMAMAGFLPFSAIYIELYYIFAS
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18300. 18406,18547. 18611,18742. 18950))
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/note="hypothetical protein"
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16027.
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                                                                                                                                               Libert Submisted (07-MAY-1999) Arabidopsis thaliana Genome Center, Department of Bology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 13699)

Scheuk, R. Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., Kham, S., Kim, C., Altafi, H., Bei, B., Chin, C., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lee, J., Ler, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission

L. Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA

On May 7, 1999 this sequence version replaced gi:4731042.
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NKKLSKEEVKQFRKAVEKDYYFQMYYDDLPIMGFIGKVDKDIKSDPSEFKYFLYKHIQ
FEILYNKDRVIEISARMDPHSLVDLTEDKEVDAEFMTTVKKETETPFEKRMEKYSMS
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VRNLLLTGCLFCGPLFLTFCFLNTVAITYTATAALPFGTIVVIVLIWTLVTSPLLVLG
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join(6881. 7029,7140. 7296,7392. 7876,7961. 8180)
//note-similar to transmembrane 9 superfamily member g114758874; similar to dbj|Av442489.1, gb|AI996021.1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
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                         (bases 1 to 132699)
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                    3 (bases 1 to 137
Ecker, J.R.
Direct Submission
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                                                             AUTHORS
TITLE
JOURNAL
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FEATURES
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Address for correspondence: kaos@kazusa.or.jp
For the latest information on annotation of this clone, please see
http://www.kazusa.or.jp/kaos/cgilbin/dgd_graph.cgirc_MCN9
Genes with similarity to proteins in the databases are described in
protein similarity are described as 'unknown protein'.

The software programs used to predict genes include: Grail
[Informatics Group, Oak Ridge National Laboratory,
http://compbio.ornl.gov/Grail-1.3/,
GENSCAN (Chris Burge, MIT, http://CRR-081.mit.edu/GENSCAN.html),
WetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of
Denmark, http://www.cbs.dtu.dk/services/netene2/) and
SplicePredictor (Volker Brendel, Stanford University,
http://gremlinl.zool.iastate.edu/cgi-bin/sp.cgi).
Genes encoding tRNAs are predicted by tRNAscan-SE
(Sean Eddy, Washington University School of Medicine, St. Louis,
http://genome.wustl.edu/eddy/tRNAscan-SE/)
This sequence may not be the entire insert of this clone. It may be
shorter because we remove overlaps between neighboring submissions.
The 5' clone is KISIBB and the 3' clone is KISIBB.
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DLTAAESSLCEETLDYENVLAEIEAEKRMKLVGHIPANNLLKTLSERSFSTADLKLEL
OLYKVRELLTRNLKLAKREVKHAMNIAOKRDSSMALLKSQLEYAHGNHPRAMKLLL
VSGIHKEAGTSGIFNNNLGCTPYQLGCYQASSVLETKALTRSCSSLRNGKPARTFSLSQ
NKSMITTYNCGLLTAASGRPLLAAQCFQASSVLETRRSCSSLRNGKPARTFSLSG
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SDLVGVFQSVEEDTSTRIDNIQVVSISGMGGIGTTTARQIFHDLVRRHFDGFAW
VCVSQQFTQKHVWQRILQELRPHDGETLQMDEYTIGCKLFQLLETGRYLLANGLESENVFR
EDWDRIKEVFPRKRGWKMLLTSRNEGVGLHADPTCLSFRARIINPKESWKLFERIVPR
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TRDSVFLKPEEARGALFADLAALLATQGHHDQAKSLITHALTLLPNNVQATVTAVYID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDQVEAANPGINVSVSKDHFDRTVTTLNIAVTWFHLYHYSKSFSILEPLFQNIQRLDE
TIALQICFLLLDISLACRDAVNFLVSVVFTGLEVLKYSPTDLFRKWKIQPISMGCF"
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similar to unknown protein"
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similar to unknown protein"
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2173. .2343)
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/note="gb|AAD55417.1
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1. .87459
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/clone="MOK9"
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             COMMENT
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Nakamura, Y., Sato, S., Asamlzu, E., Kaneko, T., Kotani, H., Miyajima, N. and Tabata, S.
Structural analysis of Arabidopsis thaliana chromosome 5. VII.
Sequence features of the regions of 1,013,767 bp covered by sixteen physically assigned Pl and TAC clones
DNA Res. 5 (5), 297-308 (1998)
                                                                                                                                                                                                                                                         SLHRTDHEQSTNISDDTLDGLHHMIHKLKTERSVRFQKVDKHACNAILLFYTDYHFDA
LAFSPLSVQLKDVAGSLFELMNLMDTSQEERTKFASVSYVVRSSESDITEPNILSSET
IEQVSAEVDCFNKLKASRMKELVMKRRTELENLCRLAHIEADTSTSLEKSTALIDSGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPRRNSAGATNNDIMTTPRSYSSHRQNGYFKEVRRLSTAPLNFVAIPKEDSVSTYTSV
CGSEPDSPLYN"
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                                                                                                                                                                ELEKECLEIYRRKVDEAANSKAQLHOSLVSIEAEIASLLAALGVFNSHSPMKAKEGSK
SLKEKLAAVRPMLEDLRLQKDERMKQFVDIKAQIEKMSGEISGYSDQLNKTMVGSLAL
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                                                                                                                                                                                                                                                                                                                                                                                     AGRGGHVNLKHAERARITVNKIPSMVDNLIKKTLLWEDETRKSFLYDGVRLYSILEDY
KLTRKQQEEEKRRYRDQKKMQDLLIKRRESIYGSKPSPRRSNSVRKTNGYNGDASVPP
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                                                                                                                                                                                                                              DEQDLTLRKLNEYQTHLRSLOKEKSDRLNKVLDYVNEVHTLCGVLGVDFGQTVSEVHP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96885 TATAATATTAAAGGAGATGATTGTACTGATTGCCTTAAACATTTCTGCTGTGAGCTTTGT 96826
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Arabidopsis thaliana genomic DNA, chromosome 5, Pl clone:MOK9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /evidence=not_experimental/product="F10B6.10"
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Nakamura, Y.
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AB015477
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40898...41036,41462...41593,41845...41871,42139...42305)
unknown protein"
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AB026658 BA000014
AB026658.1 GI:4757414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MEGSKSEAVFDSMNLNPQIFINEAINSVEDYVDQAFDFYARDAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
clone:MYF24.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gtgttgattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagag 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 71.6; DB 8; Length 87459;
Pred. No. 9.1e-09;
0; Mismatches 79; Indels 3;
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ilarity 61.7%;
Conservative C
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Matches 132;
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AB026658/c
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TITLE
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MEDLINE
REFERENCE
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TITLE
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                                                                                                                                                                                                            John(11414. 11494,11595. 11714,11801. 11858,11951. 12051, 12131. 12226,12315. 12408,12642. 12879,13005. 13362)
pir | 140675
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SLNGWEDDEVAYFTFKNVTVDNEECCKFPIFYIFSFINLIIFKIKF"
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/note="contains similarity to Ac-like transposase
gene_ld:MOK9.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VWRCSLVFSSPDKIVSVLIHLLPGLVFFTIRWWNPATFAAMHPVGTDRRVSWPYVEDK

KYLFWELVPLVYYTLWQVYLFLINVNLRRQRLLRDPEVWTSYRELSKKAEKANNKL

WQLSGLLGDONRIWYLLFQILKISAVWNGGS

FLLEVMPRQVIQKEKKKRAEWQPIEEQILHHEAVSHPTENEPKSTET"

Complement (21292. . 21564)

//octe="gene_id:MOK9.5

unknown protein:
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VPLRWIYYRFKKWHYYLLDFCYYANTIFLVDLLLYPKNEKLFWVCFSFABGPLAWAII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation-"mfvvktlarqnlafcgssgkigedgngnflsfielladfdpvwi
EHLRRFKTRATRFHYLINKIQNELTALLANEIKAMIIKKIQGARYYSVIIDCTPDISH
HEOMTVVTRQFRFRNYSAHILSFASSVKRWKIFEDKVRGLTLKPLSHTRWESHVGNTI
RNETEYEEMEAIGKEMVTYCGGLPLAVKVLGGLLANKHTASEWKRVSENIGAQIVGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MKKSRCSSFNQYEDELLCCVYLEISQDPIGSNNQSGKK"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Join(32341. .32440,32858. .33261)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene_id:MOK9.8
similar to unknown protein"
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unknown protein"
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                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
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COMMENT

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DRVFHCDGLLLCTSKLERRMYVWNPLTGETKWIQTHEEGDNFFLGYSQEDKNISCKKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FDFSTEISMHFCLLPCAKHVSGLQDKLVLTVFKGDRFALLKQSRISSNTEIWVTKDKI
NSSNNVVWLNLMTLSIPDFPSLFHQLSDISYFIHDMTLILCCDDNQTGVGCIFIARGD
LCKKIQINYVSLGFSQCVYLPSLTSVPLEFRSLQV"
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wipelspianvvvrrcskilgvsanelrdsfkoeafeslkopsleprnfleyccfral
slsvgvtghladkkfrrlffdmmvvwevpaVasqallsveedatvsleafsriaPavp
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EKILEIDGTWTTQPVLEHVGISTWPGRLILTPHSLYFPALKVVSYDFKRYHLSEDLK
OIIKPELTGPWGTRLFDKASYQSISLSEPVWBFPELKGHTRDYWLTIIQEVLYVH
RYINKKITGLARDEALSKAVLGVMRYQALQELMLTNAMRYSENLLPFNLCDQLEGGDL
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EVVVGDVVPDERAVKESRKKTEKVLAQETINGVKMGGIDTNLAVMKELMLPINGTTUN
ELSVVYNDDPFKSSVFCLLTFFIIURGMLVYVFALASLFSATFMVLTRCFSREKLMI
ELKVTAPPPNNTMBGLLAVONGISELEONIODANIVLLKFRALLFSLFPQASGKFAIA
IVVAATMMAFVPGRYLLSVVFVELFTRYSPPRASTERLIRRLREWWFSIPAAPVULL
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TLKWNENSHYKKPPSPSSSAARHHPVITHTPRITHTWRDFWALVQKICMT
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complement(9242. .10372)
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GFDLSLQSYDFSTEKFAPVSLPVPSQARSLNGANRLSVVRGEKLALLYRRDKRSKAEI
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join(12133. .1215,12398. .13249)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLKIGHRFAIFECASQAFKFIDSPEWPTLAGRGEYVSLNGNLYWTAYNEDTREHFLGS
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EKFGYVPLPPPCQVHGFEASRLSAVGDEKLSLLLVGDSTSNTELWVTSKIGEANVVSW
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16849. .17026,17139. .17476,17622. .17866,17947. .18303,
18385. .18615)
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similar to unknown protein"
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similar to unknown protein"
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LNCDIKKSLICSFPRLTRSNSTGSVAISKREMIRDINKHSSQRHGVPRPGVNPSSHMR
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KORRPRYVJSASAWSPHYQTGCLLLLDMSGEPVFPARDGARTKYWBESQGRSY
NKSWLGCEFGRRVQYTVARSDALFYTVKSTFDCSVRCILEVESLINAGAEVPGFAR
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AGSDGPRFVLASQSYVPLCDARSGVPLLKWQHDVEKPCFMDVYSLSELGVRTFESNTS
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LRETWSSLPKEILMLAFSNYSEFADVLUDKKKQSLEFLVVPEFPQLPPFLLRNPSSRS
SKWSKKEQPGVEVVGPVVPLPVLITLHEFHNGCLNSEQEFSPEAEFYNRCNQISKATR
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LKHLEVVAHKGSACKSDEVNLLYLPDDEEYKFPRRFNYLELEYLSAHRKGMLAGFLDS
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Submitted (28-APR-1999) Yasukazu Nakamura, Kazusa DNA Research
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/note="gb|AAC69119.1
                                Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-3935, Fax:81-438-52-3934)
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/codon_start=1
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/db_xref="GI:11994094"
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/note="gene_id:MYF24.3
unknown protein"
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1511. .2335
/note="gb|AAF26481.1
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Search completed: July 15, 2002, 08:28:45 Job time: 6738 sec
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                                                                                                                                                                                                                                                                                                           /evidence-not_experimental
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28416. .28471)
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YSADSSGILELHVYPANDYAADIRGTSDPYVRVOYGEKRORTKYTYTLQPKWNQ
YMEPPDDGSSLELHYKDYNTLIPTSSIGNCYVEYQGLKPNETADKWIILOGYKHGEVH
VRVTRKVYEIGRRASAGPGTPFNKALLLSNOMKQVMIKFQNLIDDGDLEGLAEALEEL
DAAGINYGAYLPTFPIFPPANPADNFLCGNQPFANFDDPLFFAPNMRSSFSSSSGF
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Elaeis guineensis microsatellite DNA, clone mEgCIR0230.
AJ271639
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complement(join(29117. .29383,29522. .29641,29726. .29869,
29953. .30004,30121. .30196,30362. .30540,30667. .30708,
30805. .30896]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               269 attcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcaccttgtg 328
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Billotte,N., Risterucci,A.M., Barcelos,E., Amblard,P. and
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similar to unknown protein"
                                                                                                                                                                                                      /note="gene_id:MYF24.9
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microsatellite; repetitive DNA
Elaeis guineensis.
Elaeis guineensis
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Unpublished
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Direct Submission
Submitted (02-FEB-2000) Billotte N., CP, Cirad, BP Avenue Agropolis
F-34032 Montpellier CEDEX 1, 34032, FRANCE
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                                                                                                                                                                                                                                                                                                                                                             /PCR_conditions="annealing temperature 52oC,1.5 mM MgCl2"
/evidence=experimental
/evidence="Forward primer"
/note="Forward primer"
/PCR_conditions="annealing temperature 52oC,1.5 mM MgCl2"
/evidence=experimental
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                                                                                                                               1. .469
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/clone="magciro0230"
/sex="allogameous"
/country="Cote d'Ivoire"
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/note="Reverse primer"
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2 (bases 1 to 469)
Billotte, N.
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July 15, 2002, 06:36:27 ; Search time 1598.68 Seconds (without alignments) 4153.741 Million cell updates/sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                         13736207 segs, 6748477542 residues
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                                                                         - nucleic search, using sw model
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492
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Maximum DB :
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb_est2:*
gb_htc:*
gb_gss:*
em_gss_hum:* em_gss_inv:* em_gss_pln:* em_gss_vrt:* em_estba:*
em_esthum:*
em_esthun:*
em_estun:*
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em_estpl:*
em_estpl:*
em_htc:*
gb_estl:* EST: * Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

A1778764 EST259643 A1778837 EST259716 AW040794 EST283658 AW09208 EST285362 AW039653 EST282101 B192259 EST42496 A1773903 EST255003 BM176887 EST35003 BM176887 EST35003 BF519667 EST457131 BG459056 00829 lea AI897534 EST266977 AI778836 EST259715 AM455311 EST311849 AI778763 EST256642 BI922710 EST542614 Description A1897534 A177836 AN77876311 A1778763 B1922710 A1778764 A1778837 AW040794 AN75220 AW092086 AW0920863 B1922592 AI773903 BM176887 AW288052 BF519667 Length DB Query Match I 333.7 311.1 31.1 31. 165.6 153 153 153 153 153 151.4 151.4 151.4 151.4 150.4 160.4 140.8

BI264661 NF118C04P BE646652 NF076H04E BG64561 NF070F02P BI263865 NF093B05P BG58453 EST486314 BM177616 saj63e02. BM17894 saj63e02. BM143408 saj63e02. BM14340 saj43f04. BM14340 saj43f04. BM18362 EST34267. BM188151 saj94040. BM188151 saj94060. BM188151 saj9606. BM188152 Saj96a06. BM188152 Saj96a06. BM188158 Saj96a06. BM18828 Saj96a06. BM188158 SAj96a06. BM188174 EST535135 BM756955 S128e04. BM756955 S128e04. BM756955 S128e04. BM756956 SST37289 A1484746 EST535136 A1484746 EST5353664 AJ407430 AJ407430		mRNA linear EST 19-MAR-2001 ZAP 2.1 two-hybrid vector cDNA one 35AE 5' similar to ORFX ission# AAF74286, mRNA sequence.	BG459056.1 GI:13382381 EST. Leafy spurge. Euphorbia esula Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots; Sosidae: eurosids I: Malolahiales: Eubhorblaceae: Euphorbia.	ed in underground adventitious buds	Lab 4, Fargo, ND 58105, USA gov	a" Lambda Hybri2A adventitious	ced (decapitated)" 148 t 2 others
0 10 10 10 10 1 4 C B B 10 11 10 C C B 10 B C B C C C C C C	B5510727 A1960277 ALIGNMENTS	610 bp 00829 leafy spurge Lambda Hybri2AP Library Euphorbia esula cDNA clone [Lycopersicon esculentum], accessi6 86459056	381 ntae; Strep liophyta; e Malbiahial	1 (bases 1 to 610) Anderson, J. V. and Horvath, D.P. Identification of mRNAs expressed Of Euphorbia esula (leafy spurge) Onpublished (2000)	Contact: Anderson JV Plants Science Research USDA/ARS, Biosciences Research Lab 1605 Albrecht Bivd., PO Box 5674, Tel: 701 239 1263 Fax: 701 239 1252 Fax: 701 239 1252	ier orb :39 rar rar	3-day induced 146 g 148
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64.78;
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1 (bases 1 to 559)
Alcala,J., Vision,T., Holt,I.E.
Lidag,F., Upton,J., White,R., Matern,A.L., Vision,T., Holt,I.E.
C.L., Nierman,W., Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley
Generation of ESTs from tomato carpel tissue
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="tomato ovary, TAMU"
/tissue_type="carpel"
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xhol; cLED - Tomato Carpel EST Library. OligodT-primed and directionally cloned cDNA in vector Lamda ZAP II with 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1897534 559 bp mRNA linear EST 18-MAY-2001 EST266977 tomato ovary, TAMU Lycopersicon esculentum cDNA clone cLED27J18, mRNA sequence.
A1897534 IG:5603436
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Starayota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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                                                                                                                                                                                                                                        270 ttcctgcttctacaggtctaaaatgagggggcaatatgatctggaagaggcaccttgtgt 329
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                                                           93 gtggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgt 152
                                 Gaps
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    Length 610;
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                Indels
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/cultivar="TA496"
/db_xref="taxon:4081"
   DB 10;
Score 165.6; DB 10;
Pred. No. 3.1e-39;
0; Mismatches 129;
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ilarity 66.0%;
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E 1 (bases 1 to 585)

S D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fulii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
L Unpublished (1999)
Contact: CUGI
Clemson University Genomics Institute
Clemson University Genomics Institute
Clemson University Genomics Contact: CUGI
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      585 bp mRNA linear EST 18-MAY-2001 EST259715 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES6K8, mRNA sequence.
A1778836
A2778836.1 GI:5276877
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cla56k8"
/clone_lib="tomato susceptible, Cornell"
                                                                                                                                                  Length 559
                                                                                                                                               Score 153; DB 9; Le
Pred. No. 2e-35;
0; Mismatches 130;
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van der Hoeven, R.S., Garvin, D., Matern, A.L., Holt, I.E., Lilang, F.,
van der Hoeven, T., Craven, M.B., Bowman, C.L., Ahn, S., Ronning, C.M.,
Fraser, C.M., Martin, G.B., Glovannoni, J.J. and Tanksley, S.D.
Generation of ESTs from tomato root tissue
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Solanales, Solanaceae, Solanum,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       585 bp mRNA linear EST 18-MAY-20 EST311849 tomato root during/after fruit set, Cornell University Lycopersicon esculentum cDNA clone cLEX10111 5', mRNA sequence. AW455311
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                Length 585;
                                                                                                                                Score 153; DB 9; Length 58
Pred. No. 2e-35;
0; Mismatches 130; Indels
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1. .585
/tissue_type="leaf"
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64.7%;
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ble, Cornell Lycopersicon esculentum cDNA
                                                                                                                                        /tissue_type="root"
/dev.stage="plants during and after fruit-set"
/dev.stage="plants during and after fruit-set"
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Xho1; supplier: Tanksley; Tissue supplied by Dave Garvin (USDA-ARS, Ithaca, NY 14850)."
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D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I, Solanales, Solanaceae, Solanum;
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/cultivar="TA496"
/db_xref="taxon:4081"
/clone="cLEX10111"
/clone_lib="tomato root during/after fruit:
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Pred. No. 2e-35;
0; Mismatches 130; Indels
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tankaley,S.D. and Giovannoni,J.
Generation of ESTs from tomato callus tissue (2001)
Contact: CUGI
                                                                                                                                                                              /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLES - Tomato Pseudomonas Susceptible EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoR and 3' end with XhoI site"
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
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                                            /organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
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/clone_lib="tomato susceptible, Cornell"
                                                                                                                                                                                                                                                                                                                 Score 153; DB 9; Length 633;
Pred. No. 2.1e-35;
0; Mismatches 130; Indels
                                                                                                                               /tissue_type="leaf"
/dev_stage="4-week old"
/lab_host="SOLR"
             Location/Qualifiers
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/clone_lib="tomato callus"
/clone_lib="tomato callus"
/tissue_type="callus"
/dab_host="25-40 days old"
/lab_host="25-40 days old"
/lab_host="15-40 days old"
/lab_host="15-40 days old"
/lab_host="5-40 days old"
/lab_host="7-10 days post-general institute; sequencing: The Institute for Genomic Research; cLEC - Cotyledons of seedlings 7-10 days post-generaliation were excised, cut at both ends and placed on MS medium with no selection. Mixed callus was harvested at 25 and 40 days and included undifferentiated masses. Tomato Callus EST Library"
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A1778764 IG:5276805
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                        Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
Institute
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larity 64.7%; Pred. No. 2.1e-35;
Conservative 0; Mismatches 130; Indels
                                                                                                                                                                                                                                1. .673
/organism="Lycopersicon esculentum"
Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:4081"
                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                             /cultivar="TA496"
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Location/Qualifiers
                                Lycopersicon esculentum
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Best Local Similarity 64.7%;
Matches 244; Conservative
                                                                                                                                                                                                                                      Clemson University
                                                                                                                                                                                                                                                                                    prime sequence.
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                                                                                                                                                                                                         Contact: CUGI
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                 tomato
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             SOURCE
ORGANISM
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                                                                                                                  AUTHORS
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AW040794
 KEYWORDS
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SET259716 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES6K8, mRNA sequence.
A1778837
A1778837.1 GI:5276878
                        1. (bases 1 to 719)

Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman
,C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannon,I.J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas susceptible tomato
Unpublished (1999)
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Asteridae; euasterids I; Solanales; Solanaceae; Solanum
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/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLE56C20"
/clone_lib="tomato susceptible, Cornell"
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/lab_host="14-week old"
                                                                                                                                                                        100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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Pred. No. 2.2e-35;
0; Mismatches 130; Indels
                                                                                                                                              Clemson University Genomics Institute
                                                                                                                                                                                                     prime sequence.
Location/Qualifiers
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Best Local Similarity 64.7%;
Matches 244; Conservative
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               Lycopersicon.
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LOCUS
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ORIGIN
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JOURNAL
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AUTHORS
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VERSION
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLES - Tomato Pseudomonas Susceptible EST Library. Directionally cloned cDNas inserted into pBlueScript SK(-) at 5' end with EcoR1 and 3' end with XhoI site"

93 c 153 g 260 t lothers
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           Tracheophyta;
                                                                                   Lycopersicon.

Lycopersicon.

(bases 1 to 720)

Liang, F. Upton, J., Matern, A.L., Vision, T., Holt, I.E.,
Liang, F. Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Fraser, C.M., Venter, J.C., Tanksley, S.D.,
Glovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas susceptible tomato
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Embryophyta; Tracnev
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     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tre
Spermatophyta, Magnoliophyta, eudicotyledons, core eudio
Asteridae, euasterids I, Solanales, Solanaceae, Solanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Lycopersicon esculentum"
/cultivar="R11-13 (Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cLE56K8"
/clone_lib="tomato susceptible, Cornell"
/tissuc_type="le4f"
/dev stage="4-week old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                100 Jordan Hall, Člemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 720;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 153; DB 9; Length 72
Pred. No. 2.2e-35;
0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLER - Tomato Pseudomonas Resistant EST Library. Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5' end with EcoR1 and 3' end with XhoI site."
                                                                                                                               EST 18-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Lycopersicon esculentum"
/cultivar="R11-12 (355::Pto in Rio Grande x Money Maker)"
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/clone="tomato resistant, Cornell"
/tssue_type="leaf"
/dev_stage="tomato"
/lab_host="Solr"
                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 620)
D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Vibrman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Giovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
Unpublished (1999)
                                                                                                                                        EST256320 tomato resistant, Cornell Lycopersicon esculentum CDNA clone cLER14122, mRNA sequence.
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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                                                                                                                               linear
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Pred. No. 6.3e-35;
0; Mismatches 131;
                                                                                                                               mRNA
                                                                                                                               620 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                            Lycopersicon esculentum
                                                                                                                                                                                                      AI775220.1 GI:5273261
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Best Local Similarity 64.5%;
Matches 243; Conservative
 467
                                    524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 prime sequence.
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451 ggagttaccatgcccc
                     Lycopersicon.
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                                    508
                                                                                                                                                                                                                                                                                                                                                     REFERENCE
AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                        RESULT 1
AI775220
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="cLET10H19"
/clone="cLET10H19"
/clone="Lib="tomato mixed elicitor, BTI"
/tissue_type="1eaf"
/dev_stage="4-6 week old plants"
/db_host="Xil-Blue MRF""
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note: "Torculated with a variety of disease response elicitors: Plants exposed to 2,6 dichloroisonicotinic acid, BTH, jasmonic acid, ethylene, fenthion, EIX, okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
                                                                                                                                                                                                                    1 (bases 1 to 544)
D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujil,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
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EST 18-MAY-2001
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                 BTI Lycopersicon esculentum cDNA
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
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Pred. No. 6e-35;
0; Mismatches 131; Indels
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 mRNA
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Contact: CUGI
Clemson University Genomics Institute
544 bp
tomato mixed elicitor,
                           clone cLET10H19, mRNA sequence.
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                                                                       AW040794.1 GI:5899548
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Local Similarity 64.5%;
nes 243; Conservative (
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D'Ascenzo,M., He,X., Lyman,J., Holt,I.E., Liang,F., Upton,J.,
Ronning,C.M., Craven,M.B., Fujii,C.Y., Bowman,C.L., Nierman,W.,
Fraser,C.M., Venter,J.C., Martin,G.B., Tanksley,S.D. and Giovannoni
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BTI Lycopersicon esculentum cDNA
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            tgccttgtatcacctttggacagatttctgaaatactaaacaaaggaacaacttcatgt 213
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clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
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/clone_lib="tomato mixed elicitor,
/tissue_type="leaf"
/dev_stage="4-6 week old plants"
/lab_host="XL1-Blue MRF'"
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Pred. No. 6.3e-35;
0; Mismatches 131;
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Best Local Similarity 64.5%;
Matches 243; Conservative
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585 bp mRNA linear EST 18-MAY-2001 cost282101 tomato mixed elicitor, BTI Lycopersicon esculentum CDNA AM039653.1 GI:5898407
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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tcctgcttctacaggtctaaaatgaggggcaatatgatctggaagaggcaccttgtgtt 330
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence
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/organism="Lycopersicon esculentum"
/cultivar="Rio Grande PtoR"
/db_xref="taxon:4081"
/clone="CLET1317"
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Unpublished (1999)
Contact: CUGI
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525 bp mRNA linear EST 18-MAX-2001 EST255003 tomato resistant, Cornell Lycopersicon esculentum cDNA AL773903 mRNA sequence.
AL773903 GI:5271944
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Directionally cloned cDNAs inserted into pBlueScript SK(-
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D' Ascenzo, M., He, X., Lyman, J., Matern, A.L., Vision, T., Holt, I.E., Liang, F., Upton, J., Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W., Frasar, W., Venter, J.C., Tanksley, S.D., Giovannoni, J.J. and Martin, G.B.
Generation of ESTs from Pseudomonas resistant tomato
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Sukaryota, Viridiplantee, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Asteridae; euasterids 1; Solanales; Solanaceae; Solanum;
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                                                                                                                                     94 tggtcaactggtctttgtcactgttttgatgaccctgctaactgtttagttactagtgtt 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   334 TCTTGTTTTTATCGTAACAAATGAGACAACAATATTTGTTGAAAAAAAGTCCTTGTGGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 AAAAATCAAGGAGTTGATATGTCAATTGGATGGCATGGAAATGTGGAGAGACAAAATCGT
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
Length 711;
                                                       Indels
                                                    0; Mismatches 140;
Score 149; DB 10;
Pred. No. 3.5e-34;
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63.2%;
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                                                       Conservative
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/db_xref="taxon:4081"
/clone="clEC77P22"
/clone=lib="comato callus"
/tlssue_type="callus"
/dev_stage="25-40 days old"
/lab_nost="X1-Blue MRF"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: EcoRI; Site_2
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Alcala,J., Vrebalov,J., White,R., Vision,T., Karamycheva,S.A., Tsai,J., Utterback,T., Van Aken,S., Ronning,C.M., Fraser,C.M., Martin,G.B., Tanksley,S.D. and Glovannoni,J.
G.B., Tanksley,S.D. and tomato callus tissue (2001)
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
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100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
This clone is available through the Clemson University Genomics
                                                                                                                                                                                                                                                                                                                                                                                                271 tcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcaccttgtgtt 330
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                                                                                                                                                                                                                                                                                                                                                 447
387
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                                                                             B1922592 711 bp mRNA linear EST 17-EST542496 tomato callus Lycopersicon esculentum cDNA clone cLEC77P22 5' end, mRNA sequence.
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This close is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
Sall: (800)-533-4363 or contact: ccu@resgen.com web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 415)
Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wuylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
Unpublic Soybean EST Project
Unpublished (1999)
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bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudloctyledons; core eudlocts;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
                                                                                            Length 525;
                                                                                                                                 Indels
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Public Soybean EST Project
end with EcoRI and 3' end c 109 g 180 t
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Pred. No. 4.8e-34;
0; Mismatches 131;
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BM176887
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240; Conservative
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Fax: 314 286 1810
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/lab_nost="NetCor: pBluescript II SK+; Site_1: ECORI; Site_2:
XhoI; The cDNA library was constructed from mRNA isolated
from 9-11 day old seedlings that were induced for HR
(hypersensitive response) by vacuum infiltrating plant
tissue with Pseudomonas syringae pv. glycinea carrying the
avrB gene (Genetics 141:1597-1604). Plant tissue (expanded
unifoliate leaves) was collected at 2, 4, 8, 12, 24, 36,
and 53 hrs after incoulation and their mRNA pooled equally
for CDNA construction. The library was prepared using the
Stratagene pBluescript II SK(+) library construction kit.
Complementary DNA was synthesized from mRNA using a primer
consisting of a poly(dT) sequence with an XhoI restriction
site. EcoRI adaptors were ligated to the blunt-ended cDNA
fragments followed by XhoI digestion. The CDNA insert is
protected from XhoI digestion via methylation during first
strand synthesis. The cDNA fragments were directionally
cloned into the EcoR-XhoI restriction site of the
pBluescript vector. The ligated cDNA fragments were
transformed into E.coli ElectroMax DHIOB host cells. Plant
care, inoculations, and library construction were
performed by Steve Clough (tila Vodkin lab, University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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Search completed: July 15, 2002, 07:56:22 Job time: 4795 sec

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Copyright (c) 1993 - 2000 Compugen Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21; Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                        25.1%; Score 12...
61.3%; Pred. No. 3.3e-32;
*ive 0; Mismatches 134; Indels
*ive 0; Mismatches 124; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC45096 standard; DNA; 523 BP
990S-0159330.
990S-0159331.
990S-0159638.
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990S-0160770.
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990S-0161405.
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Matches 217; Conservative
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21 - OCT - 1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 123.6; DB 21; Length
Pred. No. 3.5e-32;
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61.3%;
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ID AAC46412 standard; DNA; 456
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Matches 217; Conservative
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990S - 0.145918
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08-JUL-1999

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02 - AUG - 1999

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31 - J
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26-AUG-1999;
27-AUG-1999;
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18-OCT-2000 (first entry)
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18-JUN-1999;
18-JUN-1999;
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01-JUN-1999;
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10-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
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283 gattgccttaaaacatttttgctgtaacctctgtgctttgacccaacaataccgtgaactc
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                                                                                                                                                 BP.
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99US-0139452
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                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 114; DB 21; Length 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Arabidopsis genes - useful for producing transgenic
                                                                                                                                                                                                                                                                 3;
                                                                                                                                                                                                                Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pathogen response protein LSD1-interacting protein K DNA.
                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                             Score 80.2; DB 21;
Pred. No. 4.1e-17;
0; Mismatches 153;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV66762 standard; DNA; 692 BP
                                                                                                                                                                                                                16.3%;
54.3%;
990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161993.
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                                                                                                                                                                                                                                      Best Local Similarity 54.3
Matches 185; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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P-PSDB; AAW72391.
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 267
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99US-0142803.
99US-0142920.
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99US-0139492.
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99US-0132486
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99US-0139750
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99US-0140991
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99US-0128714
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                  25-FEB-1999,
05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
25-MAR-1999,
01-APR-1999,
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16-APR-1999,
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13-APR-1999,
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23-APR-1999,
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04 - MAY - 1999;

05 - MAY - 1999;

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14 - MAY - 1999;

14 - MAY - 1999;

14 - MAY - 1999;

19 - MAY - 1999;

20 - MAY - 1999;

21 - MAY - 1999;

22 - MAY - 1999;

23 - MAY - 1999;

24 - MAY - 1999;

25 - MAY - 1999;
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17-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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09-JUL-1999
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                                                                                                                           protein K (see AWV2391) of Arabidopsis thallana. LSD1 interacting genes (see AAV6755-67) were isolated from a yeast gene expression library constructed in plasmid puG4-5 using RNA from Arabidopsis leaves infected with Pseudomonas syringae. A two-hybrid system was used with LSD1 short and long open reading frames (see AAV66750-51) as bait. LSD1 (see AAW72366-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Because the inactivation of LSD1 by mutation leads to enhanced disease resistance, LSD1 partner proteins represent novel targets for engineering plants with enhanced resistance to pathogens. Thus, the invention includes all proteins (see AAW72384-96) that interact with the cell death regulator LSD1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             210 atgtgggagtagagtgcattatattgtttgctgggactgacaggattgcctagcctata 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ttcctgcttc---tacaggtctaaaatgaggggcaatatgatctggaagaggcaccttg 326
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plants which show resistance to cell death caused by pathogens or
                                                                                                             This is the nucleotide sequence of DNA encoding LSD1-interacting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 16.0%; Score 78.6; DB 19; Length 692; Best Local Similarity 54.0%; Pred. No. 1.5e-16; Matches 184; Conservative 0; Mismatches 154; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 692 BP; 219 A; 126 C; 150 G; 197 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gcttaagaaccgtggctttgatatgggaatagggtggcaag 427
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                                                                 Claim 46; Page 62; 88pp; English
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                       nerbicides
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RR 12-JUL-1999; 99US 0114297.

RR 16-JUL-1999; 99US 0114324.

RR 16-JUL-1999; 99US 0114312.

RR 19-JUL-1999; 99US 0114312.

RR 19-JUL-1999; 99US 0114313.

RR 20-JUL-1999; 99US 0114313.

RR 20-JUL-1999; 99US 0114332.

RR 20-JUL-1999; 99US 0114814.

RR 20-JUL-1999; 99US 0114514.

RR 20-JUL-1999; 99US 0114591.

RR 20-JUL-1999; 99US 0114591.

RR 10-AUG-1999; 99US 0114591.

RR 10-AUG-1999; 99US 011491.

RR 10-AUG-1999; 99US 011499.

RR 10-AUG-1999; 99US 011499.

RR 20-AUG-1999; 99US 011499.

RR 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60.4; DB 21;
Pred. No. 3.7e-10;
0; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%;
58.2%;
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990S-0156596.
990S-0157117.
990S-0157753.
990S-0157865.
990S-0158029.
990S-0158362.
990S-0159293.
990S-0159294.
990S-0159293.
990S-0159393.
990S-0159330.
990S-0159331.
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99US-0160768
99US-0160770
99US-0160814
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99US-0160989
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990S-0161360.
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Matches 106; Conservative
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29-SEP-1999, 04-0-CT-1999, 06-0-CT-1999, 07-0-CT-1999, 07-0-CT-1999, 13-0-CT-1999, 13-0-CT-1999, 14-0-CT-1999, 14-
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at 751
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Pred. No. 3.7e-10;
0; Mismatches 76;
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99US-0161359.
99US-0161361.
99US-0161920.
99US-0161992.
99US-0161993.
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Best Local Similarity 58.2%;
Matches 106; Conservative
                 99US-0154779.
99US-0155139.
99US-0155486.
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Pred. No. 4.8e-08;
0; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229 ggtactgctggagctctatacgcgttgatag
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990S - 0153070
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10.9%;
Best Local Similarity 59.6%;
Matches 90; Conservative
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Arabidopsis thaliana DNA fragment SEQ ID NO: 58448

18-OCT-2000 (first entry)

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01-JUN-10
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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Pred. No. 4e-07;
0; Mismatches 56; Indels 0
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Local Similarity 60.3%;
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PR 23-JUN-1999; 99US-0140695.

PR 26-JUN-1999; 99US-0140692.

PR 26-JUN-1999; 99US-0140823.

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PR 22-JUL-1999; 99US-0144332.

PR 23-JUL-1999; 99US-0144333.

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4.1e-07;
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Pred. No. 4.1e
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990S - 0138604
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05 MAR - 1999

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21-JUN-1999;
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.larity 64.0%; Pred. No. 1.5e-05;
Conservative 0; Mismatches 40; Indels
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ses 71; Conserv
30 - AuG - 1999
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10 - SEP - 1999
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12 - SEP - 1999
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Pred. No. 5.4e-05;
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Best Local Similarity 63.1%;
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16 - JUN - 1999;
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Pred. No. 0.0036;
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Db 1560 tgttgctgtgcccttgtacaagaactgagagaagttgagattcgtgg 1606

Search completed: July 15, 2002, 09:18:48 Job time: 4941 sec

us-09-898-659-1.rni

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Query Match 6.9
Best Local Similarity 49.2
Matches 89; Conservative
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                                                                                       July 15, 2002, 06:36:37; Search time 41.88 Seconds (without alignments) 2885.666 Million cell updates/sec
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
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US-08-998-416-254
US-08-45-742-1
US-08-36-051B-3
US-08-46-051B-3
US-08-46-908-1
US-08-871-161-1
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US-09-669-974-8
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Maximum Match 100%
Listing first 45 summaries

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length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Ulltich,, Axel
APPLICANT: Gishizsky, Mikhail
APPLICANT: Gishizsky, Mikhail
APPLICANT: Sures,, Irman G.
TITLE OF INVENTION: NOVEL MEGAKARYOCYTIC PROTEIN
TITLE OF INVENTION: TYROSINE KINASES
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: New YORK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33.8; DB 4;
Pred. No. 0.14;
); Mismatches 92;
US-08-460-402-18
US-08-078-311-20
US-08-460-402-20
US-08-460-402-17
US-08-11-17
US-08-12-202-3
US-08-184-327A-1
US-08-184-327A-1
US-08-184-327A-1
US-08-184-327A-1
US-08-184-327A-1
US-09-037-601-38
US-09-037-601-36
US-08-670-707A-36
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3R: 7683-0074-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURENTING SYSTEM: DOS
SOFTWARE: FASTESEQ VERSION 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/426,509A
FILING DATE: 21-APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: 08/232,545
FILING DATE:
APPLICATION NUMBER: 08/232,545
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5, Application US/08426509A Patent No. 6326469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: COTUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
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COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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LENGTH: 2770 base pairs
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US-08-426-509A-5
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92; Indels

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2288 AATCCCATCAGGCTGTTATTATGAAGGAATTTGATTGCTTTGCTGCACAGCAGGACCTGT 2347
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                                          aacttcatgtgggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
                                                                                                                          264 cctatattcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcacc 323
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PROTEIN TYROSINE KINASE AGONIST TITLE OF INVENTION: ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STAME: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,616
FILING DATE: 4APR-1994
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 4 APR-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00586
FILING DATE: 22-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/826935
FILING DATE: 22-JAN-1992
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-222-616-19/c
; Sequence 19, Application US/08222616
; Patent No. 5635177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Bennett, Brian D.
APPLICANT: Goeddel, David
APPLICANT: Lee, James M.
APPLICANT: Matthews, William
APPLICANT: Tsai, Siao Ping
APPLICANT: Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 82
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 7607 bases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Lee, Wendy M. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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APPLICANT: Bennet
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                 204 aacttcatgtgggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
                                                                                                      264 cctatattcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcacc 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sugen, Inc.
APPLICANT: S15 Galveston Drive
APPLICANT: S15 Galveston Drive
APPLICANT: Redwood City, California 94063-4720
APPLICANT: United States of America
APPLICANT: Wissenschaften E.V.
APPLICANT: Hofgarten Str. 2
APPLICANT: Hofgarten Str. 2
APPLICANT: Germany
TITLE OF INVENTION: Novel Megakaryocytic Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: PCT/US95/05008
FILING DATE: 24-APR-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33.8; DB 5;
Pred. No. 0.14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7683-074
TELECOMMUNICATION:
TELEPHONE: (212)790-9090
TELERA: 66141 PENNIE
TPELEX: 66141 PENNIE
INPORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,545
FILING DATE: 22-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5, Application PC/TUS9505008 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.9%;
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2770 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
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Best Local Similarity
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CITY: New York
STATE: New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TOPOLOGY: un
; MOLECULE TYPE:
PCT-US95-05008-5
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PCT-US95-05008-5
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264 cctatattcctgcttctacaggtctaaaatgaggggggaatatgatctggaagaggcacc 323
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    204 aacttcatgtyggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dumas Milne Edwards, Jean-Baptiste
APPLICANT: Dunclert, Aymeric
APPLICANT: Bougueleret, Lydie
TITLE OF INVENTION: Complementary DNAS
FILE REPERENCE: GENSET.031A
CURRENT APPLICATION NUMBER: US/09/247,155A
CURRENT FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/094,121
EARLIER APPLICATION NUMBER: 60/094,563
EARLIER APPLICATION NUMBER: 60/096,116
EARLIER FILING DATE: 1998-04-13
EARLIER FILING DATE: 1998-04-10
EARLIER FILING DATE: 1998-06
EARLIER FILING DATE: 1998-06
EARLIER FILING DATE: 1998-06
SARLIER FILING DATE: 1998-10-04
NUMBER OF SEQ ID NOS: 182
SOFTWARE: PATENTLEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: s1g_peptide
LOCATION: 61..213
OTHER INFORMATION: Von Heijne matrix
OTHER INFORMATION: score 8.1
OTHER INFORMATION: seq VCLCGFFCFPCLG/CQ
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 79, Application US/09247155A Patent No. 6312922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: polyA_signal
LOCATION: 675..680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY: polyA_site
; LOCATION: 692..703
US-09-247-155-79
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Best Local Similarity
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LOCATION: 61..405
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                                                               204 aacttcatgtgggagtagaggtgcattatattgtttgctgggactgacaggattgcctag 263
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Genentech, Inc.
APPLICANT: Genentech, Inc.
APPLICANT: Geodel, David
APPLICANT: Geodel, David
APPLICANT: Took James William
APPLICANT: Took William
APPLICANT: Took William
APPLICANT: Wood, William
TITLE OF INVENTION: PROFIEN TYROSINE KINASE AGONIST ANTIBODIES
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech T--
STREEM
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Pred. No. 0.23;
0; Mismatches 92; Indels (
                   92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CAPPLICATION DATA:
CAPPLICATION NUMBER: PCT/US95/04228
Best Local Similarity 49.2%; Pred. No. 0.23; Matches 89; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/22616
FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Wendy M. Lee
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 821P3PCT
TELECHONE: 415/25-1994
TELEFAX: 415/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 49.2'
Matches 89; Conservative
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PCT-US95-04228-19/c
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                                                                                                                                                                                                                                                                          APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 31.6; DB 4; Length 731; Pred. No. 0.39; 0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF/5-30306/A/CGC1976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        140 AATTTCTCTTTGGAAGAGCTACGAACAACATCTT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
ZIP: 27709
                                                                                                                                                                                                              Sequence 254, Application US/08998416 Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.4%;
Best Local Similarity 58.5%;
Matches 55; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: PAG1224RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                         1037 CTCGG 1033
                                              484 accag 488
                                                                                                                                                                                     US-08-998-416-254/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-998-416-254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 gaaatactaaaacaaaggaacaacttcatgtgggagtagaggtgcattatattgtttgctg 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 ggactgacaggattgcctagcctatattcctgcttctacaggtctaaaatgaggggcaa 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                304 tatgatctggaagaggcaccttgtgtttgattgtcttgtacatgtattctgtgaaccttgt 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            364 gototttgccaagaatacagagagettaagaaccgtggctttgatatgggaatagggtgg 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.6%; Score 32.6; DB 1; Length 7
Best Local Similarity 6.6%; Pred. No. 0.57;
Matches 20; Conservative 153; Mismatches 132; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                               Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHETELINGER, F.
APPLICANT: FALTKURER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 30472/114 IMMU TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
RAMB: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7218 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (703)683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 7210 LENGTH: 7210 LENGTH: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: pTZgpt-F1s
US-08-232-463-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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                                                                                                                                                                                                                                                                                                                                                                              USA
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                     RESULT 6
US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                             CITY:
STATE:
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GENERAL INFORMATION:
APPLICANT: O'Malley, Karen L
APPLICANT: Todd, Richard D
TITLE OF INVENTION: Gene Encoding the Rat Dopamine D4 Receptor
FILE REFERENCE: WU 102 CON DIV
CURRENT APPLICATION NUMBER: US/08/475,742
CURRENT APPLICATION NUMBER: US 08/261,293
EARLIER APPLICATION NUMBER: US 08/261,293
EARLIER FILING DATE: 1994-06-16
EARLIER FILING DATE: 1993-01-28
NUMBER OF SEQ ID NOS: 16
SOSTWARE: PATCHIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1963). (1965)
OTHER INFORMATION: Stop codon (TGA)
PUBLICATION INFORMATION:
AUTHORS: U'Amlley, K. L.
AUTHORS: Tang, S.
AUTHORS: C'Amlley, K. L.
TITLE: The rat dopamine D4 receptor: sequence, gene structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)..(820)
OTHER INFORMATION: 5' flanking sequence to end of exon 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
LOCATION: (445)..(447)
OTHER INFORMATION: Start codon (initiator methionine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature
LOCATION: (3264)..(3907)
OTHER INFORMATION: Exon 4 and 3' flanking sequence
                            Sequence 1, Application US/08475742
Patent No. 6121015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc_feature
LOCATION: (1)..(3907)
OTHER INFORMATION: Rat D4 Gene
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EY: misc_feature ton: (2300)..(2406) INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: intron
LOCATION: (3072)..(3263)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (2500)..(3071)
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (2407)..(2499)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE: system
JOURNAL: New Biol.
VOLUME: 4
                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 1
LENGTH: 3907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; PAGES: 1-9
; DATE: 1992
US-08-475-742-1
-08-475-742-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bradfield, Christopher Alan
APPLICANT: Dolwick, Kristin Marie
APPLICANT: Dolwick, Kristin Marie
APPLICANT: Poland, Alan
TITLE OF INVENTION: Ah Receptor cDNA and Method of
TITLE OF INVENTION: Determining Human Risks To Environmental Pollutants
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                 3109 ggggtcccgggagccgaggagggaaggggaagggtccagtttggaagggtgaaaggtgg 3168
                                                                                                                                                                                                                           3049 gagagtectgecggtggtagttggtgggttteegeeetgggaeaagagetgatagaggga 3108
                                                                                                                                                                                  331 gattgtcttgtacatgtattctgtgaaccttgtgctctttgccaagaatacagagactt 390
                                                                                                                                                                                                                                                                     391 aagaaccgiggctitgataigggaatagggiggcaagctaataiggatagacaaagccgg 450
                                                                                          271 tcctgcttctacaggtctaaaatgagggggaatatgatctggaagaggcaccttgtgtt 330
                                                  Gaps
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Score 31.6; DB 3; Length 3907;
Pred. No. 0.92;
0; Mismatches 94; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/045,806
FILING DATE: 19930408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Tilton, Fallon, Lungmus & Chestnut
100 South Wacker Drive, Suite 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08045806
Patent No. 5378822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INPORMATION:
NAME: Fentress, Susan B.
REGISTRATION NUMBER: 31.37
REFERENCE/DOCKET NUMBER: NU-9
TELECOMMUTCATION INFORMATION:
TELEPHONE: (312)-456-8000
TELEPAS: (312)-456-7776
    6.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5261 base pairs
                       Best Local Similarity 48.4
Matches 88; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 100 South Wack
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 66666-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (312)-456-777
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
US-08-045-806-3
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      Query Match
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2501 GTATTACCACAACATTCCAAATGTACAGAGCTGGACTATGGGGGGGTTTTGAACCA 2560
                                                                                                                                  2561 TCCCCATACCCCACTACTT-CTAGTTTAGAAGATTTTGTCACTTGTTTACAACTTCCTGA 2619
                                                                              126 coctgotaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctga
                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/08446908
Sequence 1, Application US/08446908
GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mochizuki, Diane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: APPLE FLOPPY disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,908
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/231,205
FILING DATE: 12-APR-1994
APPLICATION NUMBER: US 07/957,649
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 26-OCT-1988
FILING DATE: 26-OCT-1987
ATTORNEY/AGENT INPORMATION:
ANDER: COCT-1997
ATTORNEY/AGENT INPORMATION:
ANDER: COCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUTCATION INFORMATION:
TELEPRAX: (206) 587-0430
TELEPRAX: (206) 333-0644
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                      2620 AAACCAAAAGCATGGATTAAATCCA 2644
                                                                                                                                                                                 186 aatactaaacaaaggaacaacttca 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
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ANTI-SENSE: NO
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                               RESULT 11
US-08-446-908-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Bradfield, Christopher A.
APPLICANT: Bradfield, Kristin M.
APPLICANT: Carver, Lucy A.
TITLE OF INVENTION: A Receptor CDNAs and Genetically
TITLE OF INVENTION: Engineered Cells for Detecting Agonists to the AH
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Tilton, Fallon, Lungmus & Chestnut
STREET: 100 South Wacker Drive, Suite 960
2441 TACAAATCTGAATGGATTCTATGCCTTATACACAGAACTTTATTCCTGTAATCAGCCT 2500
                                                                                                                             2501 GTATTACCACAACATTCCAAATGTACAGAGCTGGACTACCCTATGGGGAGTTTTGAACCA 2560
                                                                           66 atctgcccccggcaccaccacggcgcggtggtcaactggtctttgtcactgttttgatga 125
                                                                                                                                                                            126 ccctgctaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctga 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-4002
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Tilton, Timothy L.
REGISTRATION NUMBER: 16,926
REFERENCE/DOCKET NUMBER: NU-9207-CIP
TELECOMMUNICATION INFORMATION:
TELEPAX: (312)-456-8000
TELEPAX: (312)-456-776
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/366,051B
                                                                                                                                                                                                                                                                                                                            2620 AAACCAAAAGCATGGATTAAATCCA 2644
                                                                                                                                                                                                                                                                             186 aatactaaacaaaggaacaacttca 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/08366051B
Patent No. 5650283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 5261 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acid
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic
STRANDEDNESS:
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MOLECULE TYPE:
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US-08-366-051B-3
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LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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COUNTRY: US
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY:
; LOCATION:
US-08-231-205A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-871-161-1/c
                                                                                                                                                                                                                                                                                            LOCATION:
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                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Namen, Anthony E.
APPLICANT: Namen, Anthony E.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Lupton, Stephen D.
APPLICANT: Mochlacuki, Dlane Y.
TITLE OF INVENTION: Interleukin-7 and Antibodies Reactive
TITLE OF INVENTION: Interleukin-7
TORRESPONDENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STRYE: WA
COUNTRY: US
                                                                                                                                                                                                                                        DB 1; Length 1607;
                                                                                                                                                                                                                                                                        54; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Apple Macintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Microsoft Word, Version 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/231,205A
FILING DATE: 21-APR-1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                    Query Match 6.2%; Score 30.6; DB Best Local Similarity 53.8%; Pred. No. 1.3; Matches 63; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/957,649
FILING DATE: 06-0CT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-0CT-1988
PRIOR APPLICATION NUMBER: US 07/13,566
FILING DATE: 26-0CT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEPAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08231205A Patent No. 5714585
                                                                                                                                   mat_peptide
624..1010
                                                                              sig_peptide
549..623
                                          549..1013
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NAME/KEY:
                                        LOCATION:
FEATURE:
NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                         ; LOCATION:
US-08-446-908-1
                                                                                                                                         NAME/KEY:
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254 gattgcctagcctatattcctgcttctacaggtctaaaatgagggggaatatgatctgg 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.2%; Score 30.6; DB 1; Length 1607; Best Local Similarity 53.8%; Pred. No. 1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Namen, Anthony E.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Lupton, Stephen D.
APPLICANT: Lupton, Stephen D.
APPLICANT: Interleukin-7 and Antibodies Reactive TITLE OF INVENTION: Therewith
NUMBER OF ENUMBERS: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Apple Maintosh
OPERATING SYSTEM: Apple 7.1
SOFTWARE: Mctosoft Word, Version 5.1a
CURRENT APPLICATION DATA:
FILING DATE: 09-JUN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,908
FILING DATE: 22-MAY-1995
APPLICATION NUMBER: US 08/231,205
FILING DATE: US 08/231,205
FILING DATE: US 07/957,649
FILING DATE: 06-OCT-1992
FRICH APPLICATION DATA:
APPLICATION NUMBER: US 07/511,438
FILING DATE: 13-APR-1990
FRICH APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Emmunex Corporation 51 University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/08871161
Patent No. 5965122
TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                     63; Conservative
                                                                                                                                                                                                                                                                                   mat_peptide
624..1010
                                                                                                                                                                                                                       sig_peptide
549..623
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                                                                                                                                                                               549..1013
                                                                                                                              FEATURE:
NAME/KEY: CDS
LOCATION: 549...
FEATURE:
NAME/KEY: sig_F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 51 Uni
CITY: Seattle
                                                                                                                 CLONE: muIL-7
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129 tgctaactgtttagttactagtgtttgcccttgtatcacctttggacagatttctgaaat 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: POETLET, Jane E.R.
REGISTRATION NUMBER: 33,332
REFERENCE/DOCKET NUMBER: 02356.0067-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-400
TELEPHONE: 202-408-400
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
LENGTH: 7917 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INPORMATION:
NAME: BENT, SLEPHEN A.
REGISTRATION NUMBER: 29,768
                     IMBER: US/08/167,854
10-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189 actaaacaaaggaacaacttcatgt 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         984 ATTATCTACAAAATCCACAAGATCT 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: ..... USA
ZO313-0299
COMPUTER READBLE FORM:
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS AND SOFTWARE: Patonia
                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (703)836-9300
(703)683-4109
        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best_Local Similarity 60.0
Matches 51; Conservative
                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Alexandria STATE: VA
                                              FILING DATE: 1(CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              899149
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TELEX: 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%; Score 30.6; DB 2; Length 1607; 53.8%; Pred. No. 1.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08167854
Patent No. 5952487
GENERAL INFORMATION:
APPLICANT: Sapp. Martin
APPLICANT: Cole, Stewart
APPLICANT: Mantin
APPLICANT: Maine
TITLE OF INVENTION: HPV42=Use in Diagnosis
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MADIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
APPLICATION NUMBER: US 07/255,209
FILING DATE: 07-0CT-1988
PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/113,566
FILING DATE: 26-0CT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Seese, Kathryn A.
REGISTRATION NUMBER: 32,172
REFENCE/DOCKET NUMBER: 2104-D
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 10ROFAMATION:
TELECOMMUNICATION SEQ. 10 NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mashington
                                                                                                                                                                                                                                                                                                                                                                         CDNA to mRNA
                                                                                                                                                                                                                                                                                       LENGTH: 1607 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.8
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mat_peptide
624..1010
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549..623
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                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: muIL-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-167-854-1/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; NAME/KEY;
; LOCATION:
US-08-871-161-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: V
STATE:
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| INFORMATION FOR SEQ ID NO: 14:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 718 base pairs |
| LENGTH: 718 base pairs |
| TYPE: nucleic acid |
| TOOLOGY: linear |
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Search completed: July 15, 2002, 08:28:01 Job time: 6684 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2002, 06:46:38; Search time 16.72 Seconds (without alignments) 936.756 Million cell updates/sec Run on:

US-09-898-659-2 921 1 MYPTVGYNLGLMKQPYVPPH......NMDRQSRGVTMPPYHAGMTR 163 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283138 Total number of hits satisfying chosen parameters:

283138 seqs, 96089334 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	DB ID Description	2 E96710 hypothetical prote	G96527	unknown	G96710 hypothet	E84885 hypothetical	F84788 hypothetical	T04702 hypothetical	D84556 hypothetical	T02853	F64752 probable meli	A61625	JC5571 subtilisin-li	A39490 subtilisin-like	JC5570 subtilisin-like	JN0711 protein-tyrosine	D96663	F69857	S57845 protein-	MMMSA	S40837 formate	C91231 formate	B86078 formate	2 AC0946 formate	2 I54237 protein-	1 JN0712	1 JH0771	
	Length 1	160	224	190	174	244	242	447	417	230	460	782	962	696	975	1134	232	156	1136	3084	300	300	300	300	1122	1123	1125	239
dР	Query Match L	43.8	39.7	31.3	29.4	21.0	17.8	13.4	12.5	11.3	10.7	10.4	10.0				•	9.0							8.8			
	Score	403.5		288	270.5	193	164	123	115	104.5	98.5	95.5	92.5	16	91	87.5	84	~	82.5	a	81	81	81	81	81	81	81	79.5
																											و	

protein F27J15.18 [imported] - Arabidopsis thaliana Cispecies: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96527 R;Arbeologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,

RESULT G96527

protein-tyrosine k latent transformin	laminin alpha-1 ch surface antiqen se	hypothetical prote cell-fate determin	protein-tyrosine k	hypothetical prote	glucose-1-phosphat tumor necrosis fac	nodulin-30 - kidne	retrovirus-related	uromodulin precurs	PACE4A - mouse (fr	gene PACE4 protein	MEGF6 protein – ra
S24066 A55494	S14458 A36385	T34264 A49128	158388	T34513	B84167 I54182	S42879	D44490	A30452	152527	153282	T13954
7	0 0	0 0	ч.	7	7 7	7	7	-	7	7	7
1138 1820	3075 439	2195	1124	3507	238 435	220	380	640	932	937	1574
8.8 4.8	8 8.3	8 8.7	8.1		9 0	8.0	8.0	8.0	8.0	8.0	8.0
77.5	76 75.5	75.5	75	75	74	73.5	73.5	73.5	73.5	73.5	73.5
30	35 33	34 35	36	37	308	40	41	42	43	44	45

ALIGNMENTS

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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hudhes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, A.Authors: Balzberg, S.L.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A66141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein At2945010 [imported] - Arabidopsis thaliana (C. Specials: Arabidopsis thaliana (mouse-ear cress) (C. Specials: Arabidopsis thalians (C. Specials: Arabidopsis thalians) (C. Specials: Arabidopsis (C. Spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Residues: Î-244 <STO>
A;Cross-references: GB:AE002093; NID:g4895249; PIDN:AAD32834.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:AE005173; NID:q5734717; PIDN:AAD49982.1; GSPDB:GN00141
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein F24J5.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                67 -----GTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEP 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCP---CITFGQISEILNK---- 66
       35 FAPPNYQQANVNLSVGRPWSTGLFDCQADQANAVLTTIVPCVTFGQIAEVMDEGEMTCPL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 QPY-----AEQLPQGLWTTGLCDCHEDAHICTYQNVSLRVFCLIFLLVCCLKTKCKKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.4%; Score 270.5; DB 2 37.8%; Pred. No. 1.8e-18; ive 20; Mismatches 61
                                                                                                                                                                                                                                                                   ELKNRGFDMGIGW-----QANMDRQS 149
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A;Molecule type: DNA
A;Residues: 1-174 <STO>
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A;Map position: 1
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Best Local Si
Matches 62,
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820
A; Huthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurcs, J.S.; Maiti, R.; Marziall, Rizzo, M.; Roneay, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Roneay, T.; Rowley, D.; Sakano, H.
Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Muthors: Salaberg S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Reference and analysis of chromosome 1 of the plant Arabidopsis.
A; Recession: A96562
ansen, N.F.; Hughes, B.; Huizar, L.

Atture 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MuID:21016719
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-224 <STO>
A;Cross-references: GB:AE005173; NID:g7770345; PIDN:AAF69715.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MYPTVGYNLGLMKQP-YVP------PHYVSAPG---TTTARWSTGLCHC 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
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Best Local Similarity 39.9%; Pred. No. 4.2e-20;
Matches 59; Conservative 27; Mismatches 44,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 365.5; DB ;
; Pred. No. 2.2e-27;
29; Mismatches 48
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41.8%;
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Best Local Similarity 41.8
Matches 76; Conservative
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A; Residues: 1-190 <STO>
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A; Map position: 1
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4

Gaps

21;

H.W.; Mayer, K.F.X.; Schue

3

Gaps

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Length 447;

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hypothetical protein At2g17780 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001 C;Accession: D84.56 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana. A;Reference number: A84420; MUID:20083487
A;Accession: D84556
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 WHTDLLACCSEPSLCFKTFFFPCGTLAKIATAASNRHISSAEACNELMAYSLILSC---- 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 WHADLLDCCSEPCLCLKTLFFPCGTLAKISTVATSRQISSTEVCKNLIVYSLILSC--- 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILN----KGTTSCGSRGALYCLLGLTGLP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILN----KGTTSCGSRGALYCLLGLTGLP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| | |:| | |:| | 382 CCYTCCVRRKLRKTLNITGGFIDDFLSHVMCCCCALVQELREVEIRG 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 SLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRG 134
                                                               A; Molecule type: DNA
A; Residues: 1-447 <BEV>
A; Cross-references: EMBL:AL031986
A; Experimental source: cultivar Columbia; BAC clone F4B14
R; Bevan, M.; Wedler, H.; Wambutt, R.; Hoheisel, J.; Mewes,
submitted to the Protein Sequence Database, April 1998
A; Reference number: 215418
A; Accession: T05484
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 SLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELK 131
                                                                                                                                                                                                                                                                                        A;Residues: 1-447 <BEW>
A;Cross-references: EMBL:AL022373
A;Experimental source: cultivar Columbia; BAC clone T19K4
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 123; DB 2;
; Pred. No. 0.00045;
13; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 115; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.5%; Score 11.5; 29.8%; Pred. No. 0.0024; tive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 4
A;Introns: 301/2; 340/1; 364/1; 399/3; 431/1
A;Note: F4B14.190; T19K4.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 30.8%
Matches 33; Conservative
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                   A; Reference number: 215380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-417 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pypothetical protein At2g37110 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: F84788
R;Lin, X.; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
euss, D.; Micarman, W.C.; White, O.; Elsen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
Mature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84788
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-242 <STOA
                                                                                                                                                                            4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----EAPCVDCLVHVFCEPCALCQEYRELKNRGF 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PLVPPPAAEEYGWTADGLPVSHGSVIGEPIRRNQWNSGLFTCLGRNDEFCSSDLEVCLLG 100
                                                                                                                                                                                                                                                            :: : | | | : | : | : | : | : | 49 VLPETYEPP-----SDENWITGIFGCAEDPESCRIGLFCPCVLFGRNIEAVREEIPW 100
                                                                                                                                                                                                                                                                                                                                       ------LYSCFYRSKMRG 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 SVCPCITFGQISEILNK--GTTS--CGSRGALY----CLLGLTGLPSLYSCFYRSKMRGQ 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                              Gaps
                                                                                                                                                                                                                              11 LMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK---G 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ARWSTGL--C----HCFDDPANCLVT 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 99
                                                                                                                                                                         38;
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                                                                                                                    Length 244;
                                                                                                                    Query Match 21.0%; Score 193; DB 2; Length 24. Best Local Similarity 27.7%; Pred. No. 5.7e-11; Matches 46; Conservative 23; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              QYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMD 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          161 KYHLKNAPCDHCMYHCCLHWCALCQEHREMKNHLSDTEASSSTTMD 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 164; DB 2;
; Pred. No. 3.2e-08;
17; Mismatches 65
                                                                                                                                                                                                                                                                                                                                       TTSCGSRGAL----YCLLGLTGLPS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 DMGIGWQANMDRQSRGVTMPPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            220 HPG-----FNAQSTVVVMPPIEQTMGR 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.8%;
28.8%;
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nes 60; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102 YDLE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: At2g37110
A;Map position: 2
At2945010
                                            A; Map position: 2
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Best Local Si
Matches 60;
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                   A; Gene:
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5

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53;

Length 417;

10

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Tenscallike protein precursor - fruit fly (Drosophila melanogaster)

C; Species: Drosophila melanogaster
C; Species: Drosophila melanogaster
C; Species: 21-301-1995 #sequence_revision 28-301-1995 #text_change 11-Jan-2000
C; Accession: A61655; S28463
R; Baumgartner, S.; Chiquet-Ehrismann, R.
Mech. Dev. 40, 165-176, 1993
A; Title: Ten(a), a Drosophila gene related to tenascin, shows selective transcript lo
A; Reference number: A61625, MUID:93264270
A; Accession: A61625
A; Status: preliminary
A; Molecule type: mRNA
A; Mesidues: 1-782 < BAU>
A; Mesidues: 1-782 < BAU>
A; Genetics:
A; Cross-references: FlyBase: FBgn0004446
C; Superfamily: unassigned EGF-related proteins; EGF homology
C; Superfamily: unassigned efference #status predicted <SIG>F; 497-524/Domain: EGF homology <EGF>F; 497-524/Domain: EGF
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C; Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C; Accession: JC5571
C; Accession: JC5571
J: Biochem. 121, 941-948, 1997
A; Tille: A novel human PACF4 isoform, PACF4 is an active processing protease contain A; Reference number: JC5570; MUID: 97335942
A; Reference number: JC5570; MUID: 97335942
A; Status: nucleic acid sequence not shown
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A; Experimental source: brain cerebellum
C; Comment: This enzyme is a processing protease and responsible for processing of var chiis retained intracellularly.
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DPLCSGH 537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538 GICVA-GQCYCKAGWQGEDCGTIDQQVYQCLPGCSEHGTYDLETGQCVCERHWTGPDCSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 15q26-15q26
C;Superfamily: subtilisin-like proteinase PACE4; subtilisin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 TSCGSRGALYCLLGLTGL-----PSLYSCFYRSKMRGQYDLEEAPCV-----
        Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   492 IPVGECEVPNCSSHGRCIEGECHCERGWKGPYCDQHDCL------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.4%; Score 95.5; DB 2; 22.3%; Pred. No. 0.32; iive 15; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GDB:131390; OMIM:167405
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Best Local Similarity 22.38
Matches 44; Conservative
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                 .. S
                                               168
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                                                                                                                                                                                         A; Accession: A81463
A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-230 < PYL>
A; Cross-references: 6B:AE001274; NID:93264850; PIDN:AAC24676.1; PID:92266921; GSPDB:GN00
A; Experimental source: strain MHOM/IL/81/Friedlin
A; Genetics
A; Genetics
A; Genetics
A; Genetics
A; Map position: 1
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A;Experimental source: strain K-12, substrain MG1655
                                      R;Myler, P.J.; Audleman, L.; deVos, T.; Hixson, G.; Kiser, P.; Lemley, C.; Magness, C.; Proc. Natl. Acad. Sci. U.S.A. 96, 2902-2906, 1999
A;Title: Leishmania major Friedlin chromosome 1 has an unusual distribution of protein-A;Reference number: A81455; MIID:99178987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable meliblose carrier protein yagG - Escherichia coli
N.Alternate names: probable membrane protein yagG
Species: Escherichia coli
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C.Accession: F64752
C.Bate: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999
C.Accession: F64752
B.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of Escherichia coli K-12.
A.Reference number: A64720; MUID:97426617
A.Reference number: A64720; MUID:97426617
A.Status: nucleic acid sequence not shown; translation not shown
A.Nolecule type: DNA
A.Residues: 1-460 <a href="https://doi.org/10.1007/j.com/name/">DNA
A.Residues: 1-460 <a href="https://doi.org/10.1007/j.com/">DNA
A.Residues: 1-460 <a href="https://doi.org/">DNA
A.Residues: 1-460 <a href="
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTS----CGSRGALYCL-LGLTG 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCPC 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Gene: yagG
C,Superfamily: melibiose carrier protein
F:80-96/Domain: transmembrane #status predicted <TMM1>
F:80-96/Domain: transmembrane #status predicted <TMM2>
F:155-171/Domain: transmembrane #status predicted <TMM2>
F:184-200/Domain: transmembrane #status predicted <TMM4>
F:398-314/Domain: transmembrane #status predicted <TMM5>
F:317-333/Domain: transmembrane #status predicted <TMM5>
F:317-333/Domain: transmembrane #status predicted <TMM5>
F:406-422/Domain: transmembrane #status predicted <TMM7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10.7%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | |||: | ||: ::|
192 CLPCAIAQHQREIMHQG 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 CEPCALCQEYRELKNRG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34; Conservative
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C; Accession: A81463; T02853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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Gaps 9 E-II form

55 ITFGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCV 110

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protein-tyrosine kinase (EC 2.7.1.112), receptor type tie precursor - mouse C: Species: Mus musculus (house mouse)
C: Species: Mus musculus (house mouse)
C: Date: 14-Jul-1994 #text_change 16-Jul-1999
C: Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 16-Jul-1999
C: Accession: JN0711; S3141; S57847; A48926; 165403
R: Iwama, A.: Hamaguchi, I.: Hashlyama, M.: Murayama, Y.: Yasunaga, K.; Suda, T.
Biochem Biochem. Biophys. Res. Commun. 195, 301-309, 1993
A:Title Molecular cloning and characterization of mouse TIE and TEK receptor tyrosin A:Reference number: JN0711; MUID:93371421
A:Rolecule type: mRNA
A:Residues: 1-1134 < IWA>
A:Residues: 1-1134 < IWA>
A:Residues: 1-1134 < IWA>
A:Crosak, C. A.: Andus, K.L.
Sato, T.N.: Oin, Y.: Kozak, C. A.: Andus, K.L.
Submitted to the EMBL Data Library, March 1993
                                                                                                    C;Date: 23-Sep-1997 #Sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
C;Accession: 705570
R;Mori, K.; Kii, S.; Tsuji, A.; Nagahama, M.; Imamaki, A.; Hayashi, K.; Akamatsu, T.; J. Biochem. 121, 941-948, 1997
A;Title: A novel human PACE4 isoform, PACE4E is an active processing protease contain A; Accession: JC5570; MUID:97335942
                                                  Subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form C;Species: Homo sapiens (man)
C;Spacies: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 DLEEAPCVDCLVHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMP 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                741 TAARRCRRCHKGCETCSSRAATQCL-----SCRRGFYHHQEMNTCVTLCPAGFYA 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91; DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.9%; Score ...
y 23.8%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                                                 A; Status: nucleic acid sequence not shown
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A;Residues: 1-598,'L',600-1134 <SAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44; Conservative
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A; Accession: S33141
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Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-975 <MOR>
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C; Species: Homo sapiens (man)
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Species: Homo sapiens
C; Species: Mc: Tucker, J.E.; Joh, R.; Landsberg, K.E.; Saltman, D.; Barr, P.J.
DNA Cell Biol, 10, 757-769; 1991
A; Title: Identification of a second human subtilisin-like protease gene in the fes/fps r
A; Reference number: A39490; MUD: 92075167
A; Reference number: A39490; MUD: 92075167
A; Residues: 1-969 < KIE>
A; Residues: 1-969 < KIE>
A; Residues: 1-969 < KIE>
A; Cosas references: GB: M80482; NID: G189531; PIDN: AAA59998.1; PID: g189532
C; Genetics:
C; Genetics:
A; Gene: GDB: PACE4
A; Cross references: GB: 131390; OMIM: 167405
A; Map position: 15426-15426
C; Superfamily: subtilisin-like proteinase PACE4 *status predicted <SIG>
F; 150-969/Product: serine proteinase PACE4 *status predicted
F; 150-969/Product: serine proteinase PACE4 *status predicted
F; 150-969/Product: serine proteinase PACE4 *status predicted
F; 196-434/Domain: subtilisin homology <SBT>
F; 205, 246, 420/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      subtilisin-like proprotein convertase (EC 3.4.21.-) PACE4 precursor, splice form A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   830
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTTSCGSRGALYCLLGLTGLPSLYSC----FYRSKMR------GQY-DLEEAPCVDCL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          682 STPGSANI-LQTSVCHPECGDKGCDGPNADQCLNCVHFSLGSVKTSRKCVSVCPLGYFGD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 IS----EILNKGTTSCGSRGALYCLLGLTGLPSLYSC----FYRSKMR------GQY- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      741 TAARRCRRCHKGCETCSSRAATQCL----SCRRGFYHHQEMNTCVTLCPAGFYA 790
                                                                                                                                                                                                                                                                                                                                                                                                   679 TGVCHPECGDKGCDGPNADQCLNCVHFSLGSVKTSRKCVSVCPLGYFGDTAARRCRRCHK 738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          739 GCETCSSRAATQCL----SCRRGFYHHQEMNTCVTLCPAGFYADESQKNCLKC- 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                ----VTSVCPCITFGQIS----EILNK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------VTSVCPCITFGQ 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ARGSCIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 VHVFC-----EPCALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAG 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78;
                      F;1-62/Domain: signal sequence #status predicted <SIG>
F;63:149/Domain: propeptide #status predicted <PRO>
F;196-434/Domain: subtilisin homology <SBT>
F;938-954/Domain: hydrophobic cluster #status predicted <HCL>
F;205,246,347,420/Active site: Asp, His, Asn, Ser #status predicted
F;25/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 91; DB 1; Length 969; 23.8%; Pred. No. 1.1; tive 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                            40; Indels
                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Keywords: glycoprotein; hydrolase; serine proteinase
                                                                                                                                                                                                                                            7
                                                                                                                                                                                                                                    10.0%; Score 92.5; DB 24.1%; Pred. No. 0.76; iive 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 SAPGTTTARWSTGLCH-----C---FDDPANCL--
                                                                                                                                                                                                                                                                                                                                                34 TGLCH-----C---FDDPANCL----
                                                                                                                                                                                                                                    Query Match 10.0%
Best Local Similarity 24.1%
Matches 42; Conservative
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Best Local Si
Matches 44;
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A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: mRNA
A:Cross-references: BMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611
A:Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611
B:Molecule type: Data Library, March 1993
B:Molecule the nucleocide sequence was submitted to the EMBL Data Library, March 1993
B:Molecule to nucleocide sequence was submitted to the EMBL Data Library, March 1993
B:Molecule type: March 1992
A:Title: Enhanced expression of the tie receptor tyrosine kinase in endothelial cells du A:Reference number: A48926; MUID:93043301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 221-352; 740-890 < KORS
A; Note: sequence extracted from NCBI backbone (NCBIP:118660, NCBIP:118662)
R; Korhonen, J.; Lahtinen, I.; Halmekyto, M.; Alhonen, L.; Janne, J.; Dumont, D.; Alitalc
Blood 86, 1828-1835, 1995
A; Title: Endothelial-specific gene expression directed by the tie gene promoter in vivo.
A; Reference number: 152613; MUID:95383653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.Cross-references: GB:S79346; NID:g1086920
C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type
C;Superfamily: protein-tyrosine kinase, receptor type tie; EGF homology; fibronectin type
C;Superfamily: protein-tyrosine kinase, receptor type tie #status predicted
F;1-21/Domain: signal sequence #status predicted <SIG>
F;21-1134/Product: protein-tyrosine kinase, receptor type tie #status predicted <MAT>
F;36-105/Domain: EGF homology <EGI>
F;213-253/Domain: EGF homology <EGI>
F;304-342/Domain: EGF homology <EGI>
F;363-465/Domain: Immunoglobulin homology <IM2>
F;363-465/Domain: Immunoglobulin homology <IM2>
A;Cross-references: EMBL:X71425; NID:g296610; PIDN:CAA50556.1; PID:g296611
S, Sato, T. N.; Qin, Y.; Kozak, C. A.; Audus, K.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 9355-9358, 1993
A;Title: tie-1 and tie-2 define another class of putative receptor tyrosine kinase genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;447-528/Domain: fibronectin type III repeat homology <FN3A>
F;540-629/Domain: fibronectin type III repeat homology <FN3B>
F;540-629/Domain: fibronectin type III repeat homology <FN3C>
F;542-726/Domain: fibronectin type III repeat homology <FN3C>
F;757-782/Domain: transmembrane #status predicted <TMM>
F;841-849/Region: protein kinase homology <KIN>
F;841-849/Region: protein kinase ATP-binding motif
F;43-103,370-424/Disulfide bonds: #status predicted
F;81,159,501,592,705/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;866,883,975/Active site: Lys, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
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9.5%; Score 87.5; DB 1; Length 1134;
Best Local Similarity 26.2%; Pred. No. 2.7;
Matches 34; Conservative 7; Mismatches 48; Indels 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-19 <RES>
                                                                                                                                                                                                           A; Reference number: S57845; MUID: 94022374
A; Accession: S57847
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212 GCGAGRWGPG---CVKDCPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQE 268 64 LNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVF 117 g ð ద

26 GTTTARWSTGLCHCFDDPANCLVTSVC----PCI-----TFGQISEI 63

118 CEPCALCQEY 127 ò

319 CONGGICDRF 328

Search completed: July 15, 2002, 06:48:13 Job time: 95 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

July 15, 2002, 06:47:53 ; Search time 11.96 Seconds (without alignments) 527.700 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-898-659-2 921 1 MYPTVGYNLGLMKQPYVPPH.....NMDRQSRGVTMPPYHAGWTR 163

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		P29122 homo sapien	mus ก	Q9nfh9 eurypelma c		P19137 mus musculu	esch	_	Q00174 drosophila	O70309 mus musculu		P82279 homo sapien	homo	Q02763 homo sapien	human	homo	P36941 homo sapien	nasor	P07911 homo sapien		P35419 mus musculu	Q12986 homo sapien	Q47860 erwinia her	P06401 homo sapien	P15800 rattus norv	P35444 rattus norv	Q60675 mus musculu	Q09702 schizosacch	P00748 homo sapien	Q98930 g sortilin-	771	7942	P14347 epstein-bar
SUMMARIES	ID	YAGG_ECOLI	PAC4_HUMAN	TIE1_MOUSE	HCYB_EURCA	TIE1_BOVIN	LMA1_MOUSE	FDOH_ECOLI	TIE2_MOUSE	LMA_DROME	ITB5_MOUSE	TIE1_HUMAN	CRBH_HUMAN	LMA1_HUMAN	TIE2_HUMAN	ENV_HV2KR	LMA2_HUMAN	TNR3_HUMAN	PO13_NASVI	UROM_HUMAN	PAC4_RAT	PERT_MOUSE	NFX1_HUMAN	HYIN_ERWHE	PRGR_HUMAN	LMB2_RAT	COMP_RAT	LMA2_MOUSE	NRD1_SCHPO	FA12_HUMAN	SORL_CHICK	PURA_ACTAC	٦,	UL49_EBV
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æ	Query		9.9	•	•		•	8.8	•	9.8	8.4		•	ω.	8.1	8.1	٠	8.0	8.0	٠	8.0	•	•	٠	7.8	٠	7.8	•	7.7	٠	7.7	7.7	7.7	7.6
	Score	ထ	σ	87.5	84	82.5	82.5	81	81	79.5	77.5	77.5	7	9	75	74.5			-:	•	73.5	•	٠	72	72	~	71.5	71.5	71	71	~	70.5	• 1	70
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PRGR_MOUSE	PRGR_RAT	AGRI_CHICK	CLDA_HUMAN	GLP1_CAEEL	PGBM_MOUSE	YDAO_ECOLI	MTE1_HERAU	GTR2_RAT	MUC_CANFA	ROP_DROME	Z261_HUMAN
-	Н	П	٦	٦	Н	н	Н	Н	Н	7	П
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7.6	7.6	7.6	7.5	7.5	7.5	7.4	7.4	7.4	7.4	7.4	7.4
_	70	20	69.5	69	69	68.5	68.5	68.5	89	89	68
7											

ALIGNMENTS

RESULT 1 11D 146G_ECOLI
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4;
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                                                                                                                                                                                                                            1 MYPTVGYNLGLMKQPYVPPHYVSAPGTTTA----RWSTGLCHCFDDPANCLVTS--VCPC 54
                                                                                                                                                                                                                                                                                                                                                                                                              PAC4_HUMAN STANDARD; PRT; 969 AA.
P29122; 015099; 015100; 09VEJ1; 09VEJ2; 09VEJ8; 09VEJ9; 091607; 09V469; 0015100; 09V4H1; 09VEG7; 09V469; 0015100; 09V4H1; 01-DEC-1992 (Rel. 24, Last sequence update)
01-DEC-1992 (Rel. 40, Last annotation update)
Pactro Description acid cleaving each processe pactro annotation pater annotation pater annotation pater annotation pater annotation pater basic p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identification of a second human subtilisin-like protease gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matsuda Y.;
"Identification of novel cDNAs encoding human kexin-like protease,
                                                                                                                                                                                                                                                                                              55 ITFGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identification of novel cDNAs encoding human kexin-like protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isuji A., Higashine K., Hine C., Mori K., Tamai Y., Nagamune H., Matsuda Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Placenta;
Mori K., Imamaki A., Kii S., Nagamune H., Nagahama M., Tsuji A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Higashine K., Hine C., Mori K., Tamai Y., Nagamune H.,
                                                                                                                                                                                           13;
                                                                                                                                                                                                                                                                                                                 TISSUE-Hepatoma, and Kidney;
MEDLINE-92075167; PubMed-1741956;
Kiefer M.C., Tucker J.E., Joh R., Landsberg K.E., Saltman D.,
Barr P.J.;
                                                                                                                                                         Length 460;
                                                                                                                                                                                          51; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ databases.
                                                                                       -> N (IN REF. 2).
AB600588E663C6B7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
SEQUENCE, FROM N.A. (ISOFORMS PACE4E-I AND PACE4E-II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identification of a novel PACE4 isoform, PACE4E.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        204:1381-1382(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS PACE4A-I AND PACE4B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 200:943-950(1994).
                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORMS PACE4C AND PACE4D).
TISSUE=Placenta;
                                                                                                                                                      Score 98.5; DB 1
Pred. No. 0.014;
                                                                                                                                                                                          18; Mismatches
                POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM PACE4A-II).
   POTENTIAL.
                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the fes/fps region of chromosome 15.";
DNA Cell Biol. 10:757-769(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95071480; PubMed-7980617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94235049; PubMed-8179631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            iochem. Biophys. Res. Commun.
                                                                                                       W.
                                                                                                                                                        10.7%;
29.3%;
                                                                                                       50631
                                                                                                                                                                                           34; Conservative
 200
283
329
387
426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      convertase 4) (SPC4).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
                                                                                                     460 AA;
                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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 180
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367
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                                                                   TRANSMEM
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                PAC4_HUMAN
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                                                                                                                                                                                           Matches
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CONSTITUTIVE SECRETORY PARHWAY, WITH UNIQUE RESTRICTED
DISTRIBUTION: LIKELY TO REPRESENT AN ENDOPROFEASE ACTIVITY WITHIN THE
CONSTITUTIVE SECRETORY PARHWAY, WITH UNIQUE RESTRICTED
DISTRIBUTION IN BOTH NEUROENDOCRINE AND NON-NEUROENDOCRINE TISSUES
AND CAPABLE OF CLEAVAGE AT THE RX(K/R)R CONSENGIS MOTIF.

-!- CATALYTIC ACTIVITY: RELEASE OF MATURE PROTEINS FROM THEIR
PROPROTEINS BY CLEAVAGE OF ARG-XAA-YAA-ARG-!-ZAA BONDS,
WHERE XAA CAN BE ANY AMINO ACID AND YAA IS ARG OR LYS.
-!- COFACTOR: PACEAA IS PROBABLY CALCIUM-DEPRENDET.

-!- SUBUNIT: THE PACEAA-I PRECURSOR PROTEIN SEEMS TO EXIST IN THE
RETICULUM ENDOPLASMIC AS BOTH A MONOMER AND A DIMER-SIZED COMPLEX
WHERERS MATURE PACEAA-I EXISTS ONLY AS A MONOMER, SUGGESTING THAT
PROPEDILIDE CLEAVAGE AFFECTS ITS TERTIARY OR QUATERNARY STRUCTURE.

-!- SUBCELLULAR LOCATION: PACEAA-I AND PACEA AIL ARE SECRETED.

-!- SUBCELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
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INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
INTRACELLULARLY PROBABLY THROUGH A HYDROPHOBIC CLUSTER IN THEIR C-
PACEACA-II, PACEAB MIGHT BE SECRETED.

PACEACA-II, PACEAB MIGHT BE SECRETED.

PACEACA-II, PACEAB MIGHT BE SECRETED.

PACEACA-II, PACEAB PRODUCCES BY ALTERNATIVE SPECIAL INDROPORMS PACEAB.

PACEACA-II, PACEAB PRODUCES BY ALTERNATIVE SPECIAL INDROPORMS PACEAB.

PACEACA-II, PACEAB PRODUCES BY ALTERNATIVE SPECIAL INDROPORMS PACEAB.
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TISSUE SPECIFICITY: EACH PACE4 ISOFORM EXHIBITS A UNIQUE
RESTRICTED DISTRIBUTION. PACE4A: II SE EXPRESSED IN HEART, BRAIN,
PLACENTA, LUNG, SKELETAL MUSCLES, KIDNEY, PANCREAS, BUT AT
COMPARATIVELY HIGHER LEVELS IN THE LIVER. PACE4A-II IS AT LEAST
EXPRESSED IN PLACENTA. PACE4B WAS ONLY FOUND IN THE EMBRYONIC
KIDNEY CELL LINE FROM WHICH IT WAS ISOLATED. PACE4C AND PACE4D ARE
PLACENTA AND PITUITARY. PACE4E-II IS EXPRESSED IN CEREBELLUM,
TISSUB-Cerebellum;
MEDLINE-97335942; PubMed-9192737;
MEDLINE-97335942; PubMed-9192737;
Mori K., Kii S., Tsuji A., Nagahama M., Imamaki A., Hayashi K.,
Akamatsu T., Nagamune H., Matsuda Y.;
Akamatsu T., Nagamune H., Matsuda Y.;
A novel human PACE4 isoform, PACE4E is an active processing protease
"A novel human PACE4 isoform, PACE4E is at the carboxy terminus.";
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DOMAIN: THE PROPEPTIDE DOMAIN ACTS AS AN INTRAMOLECULAR CHAPERONE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       can partly rescue the phenotype of a furin-deficient cell strain."; Biochem. J. 339:639-647(1999).
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Tsuji A., Matsuda Y.;
"Biosynthetic processing and quaternary interactions of proprotein
convertase SPC4 (PACE4).";
FEBS Lett. 434:155-159(1998).
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MEDLINE-97064242; PubMed-8906861;
Zhong M., Benjannet S., Lazure C., Munzer S., Seldah N.G.;
Functional analysis of human PACE4-A and PACE4-C isoforms:
identification of a new PACE4-CS isoform.";
FEBS Lett. 396:31-36(1996).
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            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
SIMILARITY: CONTAINS 1 HOMO B/P DOMAIN
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                                                                                                                                                                   Gaps
                                                                                                                                                                                                         ----VTSVCPCITFGQ 59
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STRAIR=BALBAC; TISSUE-Lung;
STRAIR=BALBAC; TISSUE-Lung;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
File-1 and tie-2 define another class of putative receptor tyrosine
Kinase genes expressed in early embryonic vascular system.";
Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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01-FEB-1996 (Rel. 33, Last sequence update)
116-0CT-2001 (Rel. 40, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112).
TIED OR TIE-1.
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STRALN=BALBAC; TISSUB=Liver;
MEDLINE-9371421; PubMed-8395828;
Iwama A., Hamaguchi I., Hashiyama M., Murayama Y., Yasunaga K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BALB/C; TISSUE=Bone marrow;
Krivsov A.V., Ershler M.A., Visser J.W.M., Belyavsky A.V.;
Submitted (JUN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                 47; Indels
                                                                                                                           DB 1; Length 969;
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16; Mismatches
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SEQUENCE FROM N.A.
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EMBL; AB001906; B
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EMBL; AB001908; B
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Q06806;
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CONFLICT

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            tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                           ENDOTHELIAL CELLS. SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                              DUMBAIN.
-!- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
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ATP (BY SIMILARITY).
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SMART; SM00181; EGF: 2
SMART; SM00181; EGF: 2
SMART; SM00409; IG; 1.
SMART; SM00410; IG_11ke; 1.
SMART; SM00219; TYRK: 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00102; EGF_1; 3.
PROSITE; PS00102; EGF_1; 3.
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EGF-LIKE 2.
EGF-LIKE 3.
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InterPro; IPR000561; EGF-like.
InterPro; IPR0007961; EM_pkinase.
InterPro; IPR0007961; EM_III.
InterPro; IPR003599; Ig.
InterPro; IPR003065; Ig.MRC.
InterPro; IPR003006; Ig_MRC.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00004; EGF; 2.
Pfam; PF000041; fi3; 3.
Pfam; PF000041; fi3; 3.
Pfam; PF000047; ig; 2.
Pfam; PF000069; pkinase; 1.
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EMBL; X73960; CAA52148.1; --
EMBL; S79346; --; NOT_ANNOTATED_CDS.
HSSP; P11362; 1FGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Heart;
MEDLINE-20564303; PubMed=10961996;
Voit R., Feldmaler-Fuchs G., Schweikardt T., Decker H., Burmester T.;
"Complete sequence of the 24-mer hemocyanin of the tarantula Eurypelma californicum. Structure and intramolecular evolution of the subunits.";
                                                                                                                                                                                   212 GCGAGRWGPG---CVKDCPGCLHGGVCHDHDGECVCPPGFTGTRCEQACREGRFGQSCQE 268
                                                                                                                                                                                                                        64 LNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVF 117
                                                                                                                                                                                                                                                             269 QCPGTAGC--RGLTFC-----LPDPYGCSCGSGWRGS-QCQEA-CAPDHFGADCRLQCQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 275:39339-39344(2000).
-1- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
                                                                                                                Gaps
                                                                                                                                                  --TFGQISEI 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARTHROPOS.

-1- SUBDINIT: TARANTULA HEMOCYANIN IS A 24-CHAIN POLYMER WITH SEVEN
DIFFERENT CHAINS IDENTIFIED.
-1- SUBCELLULAR LOCATION: EXTRACELLULAR.
-1- MISCELLANEOUS: THE TWO COPPER IONS BOUND EACH HAVE 3 NITROGEN
LIGANDS (PRESUDABLY CONTRIBUTED BY HIS RESIDUES) AND SHARE A
BRIDGING LIGAND (POSSIBLY CONTRIBUTED BY A TYR RESIDUE) IN
ADDITION TO BINDING OXYGEN.
-1- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eurypelma californica (American tarantula).
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
Mygalomorphae; Theraphosidae; Aphonopelma.
                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0187; HAEMOCYANIN.
PROSITE; PS00209; HEMOCYANIN.1; 1.
PROSITE; PS00210; HEMOCYANIN.2; 1.
PROSITE; PS00498; TYROSINASE_2; 1.
Transport; Oxygen transport; Copper; Glycoprotein; Hemolymph.
                                                                         Length 1134;
                                                                                                              Indels
-> L (IN REF. 1).
; 0F212ED6C50ACA0E CRC64;
                                                                                                              48;
                                                                         Score 87.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002 (Rel. 41, Created)
01-MAR-2002 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hemocyanin B chain (HcB).
                                                                                                                                                                                                                                                                                                                                                                                                                                 626 AA
                                                                                                          7; Mismatches
                                                                                                                                                26 GTTTARWSTGLCHCFDDPANCLVTSVC----PCI-
                                                                                            Pred. No.
                 1134 AA; 124698 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000896; Hemocyanin.
InterPro; IPR002227; Tyrosinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ290429; CAB89498.1; -. HSSP; P04253; 1LLA.
                                                                         9.5%;
                                                           Query Match
Best Local Similarity 26.29
                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                             118 CEPCALCQEY 127
                                                                                                                                                                                                                                                                                                                                  319 CONGGICDRF 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=29932;
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                                                                                                                                                                                                                                                                                                                                                                                                                             HCYB_EURCA
Q9NFH9;
               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          HCYB_EURCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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LMA1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
             DORNAMA MARKANA MARKAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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TISSUE-Endothelial cells;

MEDLINE-94022374; Pubmed-8415706;

Sato T.N., Qin Y., Kozak C.A., Andus K.L.;

"Tie-1 and tie-2 define another class of putative receptor tyrosine

"Tie-1 and tie-2 define another class of putative receptor tyrosine

"Tie-1 and tie-2 define another class of putative receptor.

"Tie-1 and tie-2 define another class of putative receptor.

"Tie-1 and tie-2 define another class of putative receptor.";

Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358 (1993).

--- FUNCTION: PROBABLE PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.

--- CATALYIC ACTIVITY: ATP + a protein tyrosine - ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tyrosine phosphate.
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 IGLIGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIG 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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COPPER 1 (BY SIMILARITY).

COPPER 1 (BY SIMILARITY).

COPPER 2 (BY SIMILARITY).

N.LINED (GLCNAC. . . ) (POTENTIAL).

N.LINED (GLCNAC. . . ) (POTENTIAL).

W; 17E4FB28C91F9974 CRC64;
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-!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112).
TIE OR TIE-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
-i- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 9.1%; Score 84; DB 1; Length 626; Best Local Similarity 33.8%; Pred. No. 0.57; Matches 26; Conservative 12; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1136 AA
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InterPro; IPR000719; Euk_pkinase.
                                                                                                                                                                                                                                                                                                                                 71966 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X71423; CAA50554.1; -. PIR; S32690; S32690.
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SVAILHRQDCRGVSLPP 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 WQANMDRQS-RGVTMPP 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                      172
176
203
323
327
363
311
                                                                                                                                                                                                                                                           311
315
626 AA;
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Q06805;
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      INIT_MET
DISULFID
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CARBOHYD
CARBOHYD
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TIE1_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95
          81111111118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 212 GCEAGRWGQDCTKECPGCLHGGVCH--DQDGEC----VCPPGFTGTRCEQACREGRFGQS 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 SEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 GTTTARWST------CLCHCFDDPANCLVTSVCP------CI--TFGQ1 60
                                                                                                                                                                                                                                                                                                                                                                         Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYROSINE-PROTEIN KINASE RECEPTOR TIE-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (POT
MW; EFF85804A041BB12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
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N-LINKED (GLCNAC. .) (I
N-LINKED (GLCNAC. .) (I
N-LINKED (GLCNAC. .) (I
N-LINKED (GLCNAC. .) (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Laminin alpha-1 chain precursor (Laminin A chain).
LAMAI OR LAMA-1 OR LAMA
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                                                                                                                                                                              SMART; SM00181; EGF; 2.
SWART; SM00181; EGF; 2.
SWART; SM00109; EN3; 2.
SWART; SM00109; 105; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00012; EGF_1; 3.
PROSITE; PS00108; EGF_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE 1.
EGF-LIKE 2.
EGF-LIKE 3.
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             IPR003599; Ig.
IPR003006; Ig_MHC.
IPR001245; Tyr_pkinase.
FN_III.
                                                                                                                                                                 PRINTS; PR00109; TYRKINASE
                                                                            Pfam; PF00008; EGF; 2. Pfam; PF00041; fn3; 3. Pfam; PF00047; ig; 2. Pfam; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1136 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LMA1_MOUSE
P19137;
                 InterPro;
InterPro;
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DOMAIN
TRANSMEM
DOMAIN
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MOD_RES
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                                                            interPro;
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CARBOHYD
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ProDom; PD003031; Laminin_B;
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   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     EUT. J. BLOCHEM. 177:35-45(1988).

-!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ IS THOUGHT TO MEDIATE THE ATACHMENT, MIGRATION, & ORGANIZATION OF CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
-!- SUBDINIT: LAMININ IS A COMPLEX GIYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND TO EACH OTHER BY DISJUETED BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END. THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND LAMININ-3 (S-LAMININ).
-!- SUBCELLULAR LOCATION: EXTRACEllular.
-!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPLONENT: THE ALPHA-HELLCAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

SIMILARITY: CONTAINS I LAMININ N-FERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS I LAMININ N-FERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
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SEQUENCE OF 2538-3084 FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89030693; Pubmed-3181157;
Deutzmann R., Huber J., Schmetz K.A., Oberbaeumer I., Hartl L.;
"Structural study of long arm fragments of laminin. Evidence for repetitive C-terminal sequences in the A-chain, not present in the B-chains.";
                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-89034134; PubMed=3182802;
Sasaki M., Kleinman H.K., Huber H., Deutzmann R., Yamada Y.;
"Laminin, a multidomain protein. The A chain has a unique globular domain and homology with the basement membrane proteoglycan and the
                                                                                                                                                                                                 SEQUENCE OF 1-339 FROM N.A.
MEDLINE-88225080; PubMed=3267223;
Hartl L., Oberbaeumer I., Deutzmann R.;
"The N terminus of laminin A chain is homologous to the B chains.";
Eur. J. Blochem. 173:629-635(1988).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                      J. Biol. Chem. 263:16536-16544(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, J04064; AAA39410.1; EMBL, X07737; CAA30651.1; EMBL, X13459; CAA31807.1; EMBL, M13459; CAA31807.1; EMBL, M13459; CAA31807.1; PFR; A31771; MAMSA. HSSP; P02468; JTLE. MGD, MGT:99892; Lamel. InterPro; IPR001886; Lamr. InterPro; IPR001886; Lamrin.B. InterPro; IPR001896; Laminin.B. InterPro; IPR001991; Laminin.B. InterPro; IPR001791; Laminin.B. InterPro; IPR001791; Laminin.G. Pfam; PP00052; laminin.B. 2. Pfam; PP00053; laminin.B. 2. Pfam; PP00054; laminin.B. 2. Pfam; PP00054; laminin.B. 2. Pfam; PP00054; laminin.B. 2. Pfam; PP00054; laminin.Reri. IPRNINTS; PR0011; EGFLAMININ.
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MEDLINE-99069333; PubMed-9852007;

A Benoit S., Abaibou H., Mandrand-Berthelot M.-A.;

Benoit S., Abaibou H., Mandrand-Berthelot M.-A.;

"Topological analysis of the aerobic membrane-bound formate
dehydrogenase of Escherichia coll.";

"J Bacteriol. 130:6625-6634(1998).

"J Bacteriol. 130:6625-6634(1998).

"J Bacteriol. 130:6625-6634(1998).

"J Bacteriol. 130:6725-6634(1998).

"J Bacterio
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                                                                                                                                                                                                                                                  STRAIN=K12; MEDLINE=96099298; PubMed=8522521; MEDLINE=96099298; PubMed=8522521; Mandrand-Berthelot M.-A.; Abaibou H., Pommier J., Giordano G., Mandrand-Berthelot M.-A.; Expression and characterization of the Escherichia coli fdo locus and a possible chysiological role for aerobic formate dehydrogenase.
 beta subunit) (FDH-2 beta subunit) (Aerobic formate dehydrogenase
                                           Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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R PIR, S40837, S40837.

R PSP; P00193; IFDX.

R EcoGene; EG11857; fdoH.

R InterPro; IPR001450; 4Fe4S_ferredoxin.

R Pfam; PF00037; fer4; 1.

R PRINTS; PR00135; 4FE4S_FERREDOXIN.

R PROSITE; PS00198; 4FE4S_FERREDOXIN.

R Complete proteome.
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STROUBNCE FROM N.A.
STRAIN-K12 / MG1655;
MEDLINE-93347969; PubMed-8346018;
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01-0CT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Formate dehydrogenase-0, iron-sulfur subunit (Formate dehydrogenase-0
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                                                                Gaps
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IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY). 950B40FE1A6016E7 CRC64;
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01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein Kinase receptor TIE-2) (Tyrosine-protein Kinase receptor TEE) (Tyrosine-protein Kinase receptor TEK) (Full of Interna endothelial cell Kinase) (HYK).
TEK) (Tunica interna endothelial cell Kinase) (HYK).
TEK) (Augustota: Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Musinae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sato T.N., Qin Y., Kozak C.A., Andus K.L.;
"Tiel-1 and tie-2 define another class of putative receptor tyrosine
Kinase genes expressed in early embryonic vascular system.";
Proc. Natl. Acad. Sci. US.A. 90:9355-9358(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Runting A.S., Stacker S.A., Wilks A.F.;
"Tie2, a putative protein tyrosine kinase from a new class of cell
surface receptor.";
Cowth Factors 9:99-105(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Embryonic stem cells;
MEDLINE-93129253; PubMed-1282811;
HOTITA K., Yagi T., Kohmura N., Tomooka Y., Ikawa Y., Aizawa S.;
"A novel tyrosine kinase, hyk, expressed in murine embryonic stem
                                                                                                                                50 SVCPC----ITFGQ-ISEILNKGTTSCGSRGALYCLLGLT-GLPSL-----YSCFYRS
                                                                82;
                                          8.8%; Score 81; DB 1; Length 300;
24.1%; Pred. No. 0.54;
ive 16; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Res. Commun. 189:1747-1753(1992).
                                                                                                                                                                                                                                                                                               1122 AA
                                                                                      4 TVGYNLGLMKQPYVPPHYVSAPGTTTARWS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CD-1; TISSUE-Embryonic heart;
MEDLINE-93241731; Pubmed-8386827;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-BALB/C; TISSUE-Lung;
MEDLINE-94022374; PubMed-8415706;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Lung;
MEDLINE-94031116; PubMed-8217221;
          33100 MW;
                                                               46; Conservative
                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                     137 -----MGIG 140
                                                                                                                                                                                                                                          210 NAGLYDPAGVG 220
          300 AA;
                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lochem. Biophys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             TIE2_MOUSE
Q02858;
 METAL
SEQUENCE
                                                                                                                                                                                                                                                                         RESULT 8
TIE2_MOUSE
                                                               Matches
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 7:1471-1480(1992).

-!- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
MAMMALIAN ENOOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
ENOOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: ATP + a protein tyrosine - ADP + protein tyrosine phosphate.
-i- SUBCELLIALIDAR LOCATION: Type I membrane protein.
-i- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR ENDOTHELIAL CELLS.
MEDLINE=94244487; PubMed=8187650; Schnuerch H., Risau W.; "Expression of tie-2, a member of a novel family of receptor tyrosine kinases, in the endothelial cell lineage.";
                                                                                                                                                                                                                                                                                                                                            Dumont D.J., Yamaguchi T.P., Conlon R.A., Rossant J., Breitman M.L., "Tek, a novel tyrosine kinase gene located on mouse chromosome 4, is expressed in endothelial cells and their presumptive precursors.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Clycoprotein; Phosphorylation; Multigene family.

1 18 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- DEVELOPMENTAL STAGE: EXPRESSION DETECTABLE IN DAY 8.5 EMBRYOS. -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 2 IMMUNGLOBULIN-LIKE C2-TYPE DOMAINS.
-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
EGF-LIKE 1.
EGF-LIKE 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANGIOPOIETIN 1 RECEPTOR
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MGD; MG1:38664; TEK.

InterPro; IPR000561; EGF-like.

InterPro; IPR00019; Euk_pkinase.

InterPro; IPR001961; FN_III.

InterPro; IPR001361; FN_III.

InterPro; IPR001245; TYT_pkinase.

Pfam; PF00069; pkinase; I.

PRINTS; SM00181; EGF; 2.

SMART; SM00181; EGF; 2.

SMART; SM00191; TYRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; I.

PROSITE; PS00107; PROTEIN_KINASE_ATP; I.

PROSITE; PS00119; PROTEIN_KINASE_DOM; I.

PROSITE; PS001186; EGF_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              STRAIN=CD-1; TISSUE=Embryonic heart; MEDLINE=92334855; PubMed=1630810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X71426; CAA50557.1; -.
EMBL; X67553; CAA47857.1; -.
EMBL; D13738; BAA02883.1; -.
EMBL; S67051; AAB28663.1; -.
PIR; S33142; S33142.
HSSP; P11362; 1FGK.
                                                                                                                                                            Development 119:957-968(1993).
                                                                                                                                                                                                   SEQUENCE OF 822-1122 FROM N.A.
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MEDLINE-94038678; PubMed-8223265;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 KSYVFC-----LPDPYGCSCATGWRGLQCNEACPSGYYGPDCKLRCHCTNEEICDRF-- 326
                                                                                                                                                                                                                                                                                                    PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FIHSVPRHEVP -> LHPLSAPGMKYL (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221 SRPCTTCK--NNGVCH--EDTGECICPPGFMGRTCEKACEPHTFGRTCKERCSGPEGC-- 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 RGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPC----VDCLVHVFCEPCALCQEYRE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 SAPGTTTARWSTGLCHCFDDPANCL-----VTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                                                                                                      S -> C (IN REF. 1).
A -> G (IN REF. 1 AND 4).
MLLIAILGSAGMTCITV -> DATHSHPWVWNDFASPC
                                                                                                                                                                               (POTENTIAL)
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                   (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-93049203; Pubmed-1425586;
Kusche-Gullberg M., Garrison K., Mackrell A.J., Fessler L.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         AIANSTA -> CHRQOYS (IN REF. 3).
S -> P (IN REF. 3).
W: F879623D103FFE96 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 8.8%; Score 81; DB 1; Length 1122; Local Similarity 24.1%; Pred. No. 2.1; les 32; Conservative 14; Mismatches 57; Indels
                 DOMAIN 2.
            IG-LIKE C2-TYPE DOMAIN 2. FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2. FIBRONECTIN TYPE-III 3. PROFEEN KIRASE. ATP (BY SIMILARITY).
                                                                                                                             BY SIMILARITY.

N-LINKED GLCNAC.

(FINKED GLCNA
                                                                                                                                                                                                                                                                                                                                                                                        (IN REF. 3).
N -> NV (IN REF. 3).
R -> G (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Laminin alpha chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
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925 931
1117 1117
1122 AA; 125700 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic sequence.";
EMBO J. 11:4519-4527(1992)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130 LKNRGFDMGIGWQ 142
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Q00174;
                                                                                                                                 ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
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                                              DOMAIN
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NP_BIND
BINDING
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              DOMAIN
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CC --- SUBBONIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND CC TO EACH OTHER BY DISCULFIDE BONDS INTO A CROSS-SHAPED MOLECULE COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.

CC --- SUBCELLULAR LOCATION: EXTRACELLULAR; FOUND IN THE BASEMENT MEMBRANES (MAADOR COMPONENT).

CC --- TISSUE SPECIFICITY: NEWLY FORMED MESODERM AND LATER PROMINENTLY EXPRESSED IN HEMOCYTES, WHICH ALSO SYNHHESIZE COLLAGEN IV.

CC --- DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO

CC --- DEVELOPMENTAL STAGE: DURING MORPHOGENESIS, MOSTLY IN EMBRYO

CC --- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT

WITH OTHER LAMININ CHAINS TO FORM A COLLED COLL STRUCTURE.

CC --- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN VI).

CC --- SIMILARITY: CONTAINS 1 LAMININ DOMAIN IV (DOMAIN IV' IS NOT SIMILARITY: CONTAINS 5 LAMININ DOMAIN IV).

CC --- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@iib.ch).
Henchcliffe C., Garcia-Alonso L., Tang J., Goodman C.S.;
"Genetic analysis of laminin A reveals diverse functions during
morphogenesis in Drosophila.";
Development 118:325-337(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Flysase; FBgn002226; LanA.
InterPro; IPR00186; LanA.
InterPro; IPR00186; Laminin_EG.
InterPro; IPR00184; Laminin_EG.
InterPro; IPR001249; Laminin_EG.
InterPro; IPR001230; Prenyltn.
Pfam; PF00052; laminin_E9; I.
Pfam; PF00054; laminin_E9; Pfam; PF00054; laminin_E9; 20.
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Pfam; PF00055; laminin_Nterm; 1
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ProDom; PD003031; Laminin_B; 1.
                                                                                                                                                  SEQUENCE OF 1762-3712 FROM N.A
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SMART; SM00001; EGF_like; 1.
SMART; SM00281; LamB; 1.
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SMART; SM00136; LamNT; 1
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MEDLINE-98198405; PubMed-9531507;
Zhang H., Tan S.M., Lu J.;
"cDNA cloining reveals two mouse beta5 integrin transcripts distinct in
cytoplasmic domains as a result of alternative splicing.";
Biochem. J. 331:631-637(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AFQ-----PPSCDS-----CAYGY/GYPNCRECECNLNGTNGYHCEAESGQQCPCKI 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 FGQISEILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLE-----EAPCVD 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 TVGYNLGLMKQPYVPP---HY----VSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCIT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 3712;
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ITB5_MOUSE STANDARD; PRT; 798 AA.
C 070309; 070308; 088347;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-O
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                     8.6%;
26.0%;
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14; Conservative
                     : 1: ||
473 NFAGAYCKOCA 483
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                     Query ...
Best Local Similar
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PROSITE; PS01186; EGF_2; 5.
PROSITE; PS01248; LAMININ_TYPE_EGF; 19.
PROSITE; PS50025; LAM_G_DOMAIN, 5.
Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                   LAMININ EGF-LIKE 12.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 13.
LAMININ EGF-LIKE 14.
LAMININ EGF-LIKE 15.
LAMININ EGF-LIKE 16.
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LAMININ EGF-LIKE 21.
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LAMININ G-LIKE 2.
LAMININ G-LIKE 3.
LAMININ G-LIKE 5.
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
                                                                                                       LAMININ ALPHA CHAIN.
LAMININ ALPHA CHAIN.
LAMININ EGF-LIKE 1.
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4.
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LAMININ EGF-LIKE 9.
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics. Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modifiad and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
      Feng X., Teitelbaum S.L., Quiroz M.E., Towler D.A., Ross F.P.; "Cloning of the murine beta5 integrin subunit promoter. Identification of a novel sequence mediating granulocyte-macrophage colony-stimulating factor-dependent repression of beta5 integrin gene
                                    transcription..;
J. Blol. Chem. 274:1366-1374(1999)
J. Blol. Chem. 274:1366-1374(1999)
J. FUNCTION: INTEGRIN ALPHA-V/BETA-5 IS A RECEPTOR FOR FIBRONECTIN.
IT RECOGNIZES THE SEQUENCE F.G-D IT ITS LIGAND.
-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-5
                                                                           ASSOCIATES WITH ALPHA V.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; BETA-5A (SHOWN HERE) AND BETA-5B; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE INTECRIN BETA CHAIN FAMILY.
SIMILARITY: CONTAINS I VWFA-LIKE DOMAIN.
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MEDLINE-99098874; PubMed-9880508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          BY
BY
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InterPro; IPR000561; EGF-11ke.
InterPro; IPR002369; Integrin_B.
InterPro; IPR003659; PSI.
InterPro; IPR002035; VWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF043257; AAC40110.1; -.
EMBL; AF042325; AAC40109.1; -.
EMBL; AF022110; AAD08782.1; -.
HSSP; P04355; ZMRT.
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Submitted (JUL-1993) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PROBABLE PROTEIN TYROSINE-KINASE TRANSMEMBRANE RECEPTOR.
-!- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 LIGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVH-----VFC-----EPCALCQEYRE 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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15-JUL-1999 (Rel. 38, Last annotation update)
Tyrosine-protein kinase receptor TIE-1 precursor (EC 2.7.1.112)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.4%; Score 77.5; DB 1; Length 798; 26.0%; Pred. No. 3.3; tive 10; Mismatches 48; Indels 3
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-> R (IN REF. 2).
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MEDLINE-92195316; Pubmed-1312667;
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01-JUN-1994 (Rel. 29, Last seq
15-JUL-1999 (Rel. 38, Last anno
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Matches 32; Conservative
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                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
W; 3B42BE33678C58A1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding; Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYROSINE-PROTEIN KINASE RECEPTOR TIE-1.
                                             SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                        SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS. SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS. SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.
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SMART; SMO0181; EGF; 2.
SMART; SMO019; Tyrkc; 1.
PROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00022; EGF_1; 3.
PROSITE; PS01186; EGF_2; 3.
                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003961; Fu_III.
InterPro; IPR003961; Fy_III.
InterPro; IPR001306; Ig_MHC.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000041; fin3; 3.
Pfam; PF000041; fin3; 3.
Pfam; PF000641; fig; 2.
Pfam; PF00064; jg; 2.
Pfam; PF00069; pkinase; 1.
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161 161
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1007 1007
1138 AA; 125089 M
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MIM; 600222; -.
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Best Local Similarity 24.69
                               ENDOTHELIAL CELLS.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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-! SUBCELLULAR LOCATION: Extracellular (Potential).

-! SUBCELLULAR LOCATION: Extracellular (Potential).

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: PREFERENTIAL EXPRESSION IN RETINA, ALSO

-! TISSUE SPECIFICITY: A NATOSOMAL RECESSIVE CONDITION WHICH IS

CHARACTERIZED BY NIGHT BELINDRESS FROM EARLY CHILDHOOD AND

PROGRESSIVE VISUAL FIELD LOSS. THERE IS GENERAL LOSS OF RETINAL

PROGRESSIVE VISUAL FIRELD LOSS. THERE THAN AND PATIENTS EXPERIENCE

SEVERE VISUAL IMPAIRMENT BEFORE THE AGE OF TWENTY.

-! DISEASE: Defects in CRB1 are a cause of a form of Leber congenital
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND VARIANTS RP12 V-161; W-250; M-745; C-764; Y-948; Y-1014 AND P-1071.
TISSUB-Retina, and Fetal brain;
MEDLINE-99438399; PubMed-10508521;
den Hollander A.L., ten Brink J.B., de Kok Y.J.M., van Soest S., van den Born L.I., van Driel M.A., van de Pol D.J.R., Payne A.M., Bhattacharya S.S., Kellner U., Hoyng C.B., Westerveld A., Brunner H.G., Bleeker-Wagemakers E.M., Deutman A.F.,
Heckenlively J.R., Cremers F.P.M., Bergen A.A.B.;
"Mutations in a human homologue of drosophila crumbs cause retinitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Leber congenital analysis and retinitis pigmentosa with Coats-like exudative vasculopathy are associated with mutations in the crumbs homologue I (CRBI) gene.";
Am. J. Hum. Genet. 69:198-203(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-21303018; PubMed-11389483; den Hollander A.I., Heckenlively J.R., van den Born L.I., de Kok Y.J.M., van der Velde-Visser S.D., Keliner U., Jurklies B., van Schooneveld M.J., Blankenagel A., Rohrschneider K., Wissinger B. Cruysberg J.R.M., Deutman A.F., Brunner H.G., Apfelstedt-Sylla E., Hoyng C.B., Cremers F.P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WWW="http://www.retina-international.com/sci-news/crblmut.htm".
                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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NOTE=Retina International's Scientific Newsletter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: CONTAINS 15 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 3 LAMININ G-LIKE DOMAINS.
-!- DATABASE: NAME=Mutations of the CRB1 qene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANT LCA ARG-1100, AND VARIANT RP ARG-1181.
                                                                   16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
                                                                                                                                              Crumbs protein homolog 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nat. Genet. 23:217-221(1999).
                           STANDARD;
                                                                                                                                                                                             Homo sapiens (Human)
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                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                      CRBH_HUMAN
CRBH_HUMAN
                                                                                                                                                                       CRB1.
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48; Indels 41; Gaps

8.4%; Score 77.5; DB 1; Length 1138; 24.6%; Pred. No. 4.8; tive 9; Mismatches 48; Indels 41

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EGF-LIKE 9.

LAMINING G-LIKE 1.

EGF-LIKE 10.

LAMINING G-LIKE 3.

EGF-LIKE 11.

EGF-LIKE 11.

EGF-LIKE 12.

EGF-LIKE 13.

EGF-LIKE 14.

EGF-LIKE 14.

EGF-LIKE 15.

CALCIUM-BINDING (POTENTIAL).

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CRUMBS PROTEIN HOMOLOG 1.
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EGF-LIKE 4, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
EGF-LIKE 7.
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   MEDLINE—89280632; PubMed=2733383;
MEDLINE—89280632; PubMed=2733383;
AGENED D., Sasaki T., Fazio M., Peltonen J., Jaakkola S.,
Alsen D., Magayoshi T., Fazio M., Peltonen J., Jaakkola S.,
Alsen D., Magayoshi T., Fazio M., Peltonen J., Deutzmann R.,
Alsen D., Sasaki T., Kuivaniemi H., Chu M.L., Deutzmann R.,
Timpl R., Uitto J.;
Thinan laminin: cloning and sequence analysis of cDNAs encoding A, Bl
Atim and cultured cells.;
Atim and cultured cells.;
Lab. Invest. 60:77-782(1989).
CI-FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ OF
CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
CI-SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
COMPRISING ONE LONG & THREE SHORY ARMS WITH GLOBULES AT EACH BND.
TO EACH OTHER BY DISCULPIDE BNDS INTO A CROSS-SHAPED MOLECULE
COMPRISING ONE LONG & THREE SHORY ARMS WITH GLOBULES AT EACH BND.
THE ALPHA-1 CHAIN IS A SUBUNIT OF LAMININ-1 (EHS LAMININ) AND
CI-SUBCELLULAR LOCATION: EXTRACELLULAR.
CI-SUBCELLULAR.
COMPANIENT MATRIX ENDED MATRIX
CI-SUBCELLULAR LOCATION: EXTRACELLULAR.
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COMPANIENT MATRIX ENDED MATRIX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPONENT).

DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.

DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.

SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).

SIMILARITY: CONTAINS 17 LAMININ BGF-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.

SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
   ---EAPC---- 109
                       154 SSPCQNGAVCQDGIDG----YSCFCVPGYQGRHCDLEVDECASDPCKNEATCLNEIGRYT 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-2628 FROM N.A.
MEDLINE-91264789; PubMed=2049067;
Nissinen M., Vuolteenaho R., Boot-Handford R., Kallunki P.,
Tryggvason K.;
"Pringayason K.;
"Pringayason K.;
"Pringayason K.;
"Pringayason K.;
"In human tissues.";
                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-9133420; Pubmed-1714537;
Haaparanta_T., Uitto J., Ruoslahti E., Engvall E.;
"Molecular cloning of the cDNA encoding human laminin A chain.";
Matrix 11:151-160(1991).
                                                                                                                                                                                                                            01-MXY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Laminin alpha-1 chain precursor (Laminin A chain).
70 SCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQY-DLE----
                                                                                                                                                                                               PRT; 3075 AA
                                                                     110 ------VDCLVHV---FCEPC---ALCQE 126
                                                                                           210 CICPHNYSGVNCELEIDECWSQPCLNGATCQD 241
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                                                                                                                                                                                                 STANDARD;
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CC or send an email to licenseeliab-sib.ch).

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CC REBL. N85331, CAM4448.1; ...

RES. 514458; 514458.

RES. 514458; 514458.

RES. 514458; 154458.

RES. 514458.

RES. 51444.

RES. 51448.

RES. 51
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tyrosine phosphate.
SUBCELLUIAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: PREDOMINATLY EXPRESSED IN ENDOTHELIAL CELLS
AND THEIR PROGENITORS, THE ANGIOBLASTS. HAS BEEN DIRECTLY FOUND
IN PLACENTA AND LUNG, WITH A LOWER LEVEL IN UMBILICAL VEIN
ENDOTHELIAL CELLS, BRAIN AND KIDNEY.
DISEASE: DEFECTS IN TEK ARE A CAUSE OF DOMINANTLY INHERITED VENOUS
MALFORMATIONS (VMCM1), AN ERROR OF VASCULAR MORPHOGENESIS
CHARACTERIZED BY DILATED, SERPICINOUS CHANNELS.
SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
                                                                                                                                                                                                                                                                                                                        MEDLINE-97134665; PubMed-8980225; Vikkula M., Boon L.M., Carraway K.L. III, Calvert J.T., Diamonti A.J., Gommerov B., Pasyk K.A., Marchuk D.A., Warman M.L., Cantley L.C., Mulliken J.B., Olse B.R.;
                     -----GCTDEGQCHCVPGVAG-KRCDRCAH-----GFYAYQDGSCTPCDFTQNTCD 1008
                                                                                                                                                                                                                                                                                                                                                                             63 ILNKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGOYDLEEAPCVDC-LVHV--FCE 119
                                                                                                                                                                                                                                                                     Ziegler S.F., Bird T.A., Schneringer J.A., Schooley K.A., Baum P.R., "Molecular cloning and characterization of a novel receptor protein
                                                                                                               01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Angiopoietin 1 receptor precursor (EC 2.7.1.112) (Tyrosine-protein kinase receptor TIE-2) (Tyrosine-protein kinase receptor TEF) (FIL TEK) (Tunica interna endothelial cell kinase).
                                                                                                                                                                                                                                                                                                                                                           "Vascular dysmorphogenesis caused by an activating mutation in the receptor tyrosine kinase TIE2."; Cell 87:1181-1190(1996).
                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                              1009 PETGECVCPPHTQGGKCEECED----GHWGYDAEVGCQA 1043
                                              -----CALCQEYRELKNRGFDMGIGWQA 143
                                                                                                           PRT; 1124 AA
                                                                                                                                                                                                                                                                                       tyrosine kinase from human placenta.";
Oncogene 8:663-670(1993).
                                                                                                                                                                                                                                                  TISSUE-Placenta;
MEDLINE-93173509; PubMed-8382358;
                                                                                                           STANDARD;
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90 LLGLTGLPSLYSCFYRSKMRGQYDLEEAPC-----VDCLVHVFCEPCALCQEYRELKNR 133
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Q74126;
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between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                      Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain; Glycoprotein; Phosphorylation; Multigene family; Disease mutation. SIGNAL
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EXTRACELLULAR (POTENTIAL).
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                                                                                                                                 InterPro; IPR000561; EGF-11ke.
InterPro; IPR00079; Euk_pkinase.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR0001961; Fu_III.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF000061; EGF; 1.
Pfam; PF000061; EGF; 1.
Pfam; PF00069; PKINASE.
SWART; SW00181; EGF; 2.
SWART; SW00001; EGF_11ke; 1.
SWART; SW00001; EGF_11ke; 1.
SWART; SW00001; EGF_11ke; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00107; PROTEIN_KINASE_DOM; 1.
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MIM; 60021; -. MIM; 600195; -.
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-----LPDPYGCSCATGWKG-LQCNEA-CHPGFYGPDCKLRCSCNNGEMCDRF----Q 327
                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AIDS; Coat protein; Polyprotein; Glycoprotein; Transmembrane; Signal.

SIGNAL 1 19 POTENTIAL.
                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
Kraus G.K., Talbott R., Leavitt M., Luznick L., Schmidt A.,
Badel P., Bartz C., Morton W., Wong-Staal F., Looney D.J.;
Submitted (APR-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   Human immunodeficiency virus type 2 (isolate KR) (HIV-2).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBL_TaxID=73484;
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EXTERIOR MEMBRANE GLYCOPROI
TRANSMEMBRANE GLYCOPROTEIN.
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InterPro; IPR000328; Env_GP41.
InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
Pfam; PF00517; GP41, 1.
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857 AA;
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P94032 arabidopsis
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09rlkl rattus norv
09rlk0 rattus norv
09wts5 mus musculu
09rlk2 rattus norv
09caj7 arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A. Frary A., Grandillo S., van der Knaap E., Frary A., Alpert K.B., Tanksley S.D.; Liu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.; "fw2.2: a quantitative trait locus key to the evolution of tomato fruit size.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon pennellii (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Peprantophyta; Nagnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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EMBL; AF261775; AAF74287.1; -.
SEQUENCE 163 AA; 18062 MW; 0628795F184B4869 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CALCQEYRELKNRGFDMGIGWQANMDRQSRGVTMPPYHAGMTR 163
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 921; DB 10;
ilarity 100.0%; Pred. No. 1.3e-98;
Conservative 0; Mismatches 0;
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            P94032
0952C8
0952C8
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09M2F1
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Query Match
Best Local Similarity
Matches 163; Conserv
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                                                                                                                                                                                    1 MYPTVGYNLGLMKQPYVPPH.......NMDRQSRGVTMPPYHAGMTR 163
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Q9shd7
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Compugen Ltd
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                                                                                                                                                                                                                                                              562222 seqs, 172994929 residues
            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                               summaries
                                                                      protein search, using sw model
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09SX24
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Q9FPE1
Q9SHD7
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Gapop 10.0 , Gapext 0.5
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sp_unclassified:*
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sp_human:*
sp_invertebrate:*
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921 899 433 403.5 378 378 385.5 358.5 358.5 378.5 299.5 288 270.5 193 1193

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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
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Best Local Similarity
Matches 80; Conserv
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Q9SX24;
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                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Frary A., Nesbitt T.Clint, Frary A., Grandillo S., van der Knaap E.
Copp B., Llu J., Meller J., Elber R., Alpert K.B., Tanksley S.D.;
"fw2.2: a quantitative trait locus key to the evolution of tomato fruit size.";
                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eddicotyledons; core eudicots; Asteridae; euasterida I; Solanales; Solanaceae; Solanum.
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.6%; Score 899; DB 10; Length 10
98.2%; Pred. No. 4.6e-96;
Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL: AF261774; AAF74286.1; -.
SEQUENCE 163 AA; 18061 MW; AA46EA140B7A8803 CRC64;
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Last annotation update)
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                                                                                                  Q9LKV7;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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Submitted (FEB-1999)
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Matches 160;
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Rhan S., Kim C., Altafil H., Bei B., Chin C., Chiou J., Choi E., Chan S., Kim C., Altafil H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalaz A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., A. Lee J., Lenz C., Li J., Liu A., Ethan P., Sakano H., Schwartz J., Southwick A., Anaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.

R EMBL; AC006917; AAF79235.1; -
R InterPro; IPR00152; Asz_hydroxyl.
R PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
R PROSITE: PS00010; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-CV. COLUMBIA;
Vysotskaia V.S. Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J.M., Li J., Gonzalez A., Liu R., Liu K., Vaysberg M., Sakano H.,
Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Howng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F2475 from Arabidopsis thaliana chromosome 1.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 GTTSCGSRGALYCLL-GLTGL--PSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCAL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 ALYCLLG-LTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 ALYALIAVVTGCACIYSCFYRGKMRAQYNIKGDDCTDCLKHFCCELCSLTQQYRELKHRG 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16 YVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRG 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8 NLGLMKQPYVPPHYVSAPGTTTAR-WSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 152;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 433; DB 10;
Pred. No. 3.3e-42;
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llarity 48.5%; Pred. No. 9e-39;
Conservative 27; Mismatches
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47.0%; Score 433; DB
Best Local Similarity 51.0%; Pred. No. 3.3e
Matches 78; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120 YDMSLGWAGNVEROQNQGGVAMGAPVFOGGMTR 152
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SEQUENCE FROM N.A.
TISSUB-GERMINATING PETUNIA POLLEN TREATED WITH KAEMPFEROL;
MEDLINE-20317212; PubMed-10859200;
GUYON V.N., Astwood J.D., Ganner E.C., Dunker A.K., Taylor L.P.;
Isolation and characterization of cDNAs expressed in the early stages of flavonol-induced pollen germination in petunia.";
Plant Physiol. 123:699-710(2000).
EMBL; AF049928; AAD02254-1;
SEQUENCE 145 AA; 16302 MW; 9835DB8F584E9344 CRC64;
                                                                                         Petunia hybrida (Petunia).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Petunia.
 (TrEMBLrel. 10, TrEMBLrel. 10, TremBLrel. 19,
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Best Local Similarity 41.8
Matches 76; Conservative
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hes 74; Conserv
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                                       01-DEC-2001
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   01-MAY-1999
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Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Cheuk R., Shinn P., Brooks S., Buehler E., Chiou J., Choi E.,
Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
Lee J., Lanz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,
Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
Theologis A., Ecker J.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC006917; AAF79233.1; -.
SEQUENCE 151 AA: 16503 MW; 7D17F5B8CA5E9368 CRC64;
54 GSTSCGVSGAMYMIIFMLIGYGGSSLYSCFYRTKLRAQYNLKERPCCDCCVHFCCEPCAL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74 RGALYCLLGL-TGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafi H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen E., Huizar L., Kremenetskala I., Lenz C., Li J., Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskala V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosió
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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48.4%; Pred. No. 9.6e-39;
Live 21; Mismatches 47; Indels 1:
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Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
                                     124 COEYRELK-NRGFDMGIGWQANMDRQSR----GVTMPPYHAGMTR 163
                                                        114 CQEYRQLQHNRDLDLVIGWHGNMERHARLAASTPSAPPLQAPMSR 158
                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
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                                                                                                                                                                       PRT;
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Matches 75; Conservative
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Q92TM8;
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Q92TM8
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Q9LQU2
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74 RGALYCLLGL--TGLPSL-YSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYREL 130
                                                                                                                                                                                                                                                                                                                                  51 SGTVYLLVYLVTSGFGCCWYSCFYRSKLRNQYYLDEKPCSDLCTHCCCEYCALCQEYREL 110
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                       Gaps
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                                                                                                                                                                           1 MYPTVGYNLGLMKQP-YVP-------PHYVSAPG---TTTARWSTGLCHC 39
                                                                                                                                     14 QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS
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      Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
F27J15.18.
41.0%; Score 378; DB 10;
47.7%; Pred. No. 7.1e-36;
tive 19; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                     131 KNRGFDMGIGWQANMD--RQSRGVTMPPYHAGMTR 163
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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
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                core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90 YSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQS 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 FSCTYRTKIRSKFGLPESPTSDCVTHFFCECCALCOEHRELKTRGLDPSIGWSGNMOR-- 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 OWISGLESCMEDSETACLICECPCVIFGRIADISDEGRIGGGRGGVFGLICCVVGLPCL 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGLPSL 89
                                                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 3. I. Seque
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                    Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S., Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kaneko T., Kato T., Asamizu E., Tabata to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 133;
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                Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-0c7-2000 (TrEMBLrel. 15, Last sequence update)
01-0c7-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, P1 CLONE: MYF24.
Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 347; DB 10;
; Pred. No. 2.5e-32;
21; Mismatches 38;
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MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                    MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                    Jones.";
JDNA Res. 7:131-135(2000).
EMBL; AB026658; BAB01113.1; -.
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EMBL; AB02658; BAB01111.1; -.
SEQUENCE 184 AA; 20103 MW;
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Best Local Similarity
Matches 61; Conserv
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Best Local Similarity
Matches 62; Conserv
                                                                                             SEQUENCE FROM N.A.
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                                                                                                                    STRAIN-COLUMBIA;
                                                       NCBI_TaxID=3702;
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Q9LS45;
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                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
GENOMIC DNA, CHROMOSOME 3, Pl CLONE: MYF24.
Arabidopsis thaliana (Mouse-ear cress).
Rukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 RGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNRGFDMGIGWQANMDRQSRG----VTM 154
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                95
                                                       40 FDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRGALYCLL-GLTGLPSLYSCFYRSKM 98
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:|| | |::|| || 39 IYPNNG---GVVNQPWRPGPPTYINQSATFNQPYGVSMAGPVHTQPSNWTSGLFDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38; Indels
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!: 9D07D3F21AA0BF84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09LS43 PRELIMINARY; PRT; 133 AA. 09LS43; 01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2000 (TrEMBLrel. 15, Last annotation update) GENOMIC DNA, CHROMOSOME 3, Pl CLONE: MYF24. Arabidopsis thaliana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                     184 AA.
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MEDLINE-20277480; PubMed-10819329;
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AB026658; BAB01112.1; -.
NCE 184 AA; 20150 MW;
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Matches 59;
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Best Local S
Matches 62
                                                      SEQUENCE
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J., Wu D.,
Malti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
                                                                  S DEGATPCATAGLLYGALFFTGASFVYSYMFRARIRKKRGLPDAPAPDWITHLYCMPFALC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 QISEILNKGTTSCGSRGALYCLL----GLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 PTVGYNLGLMKQPYVPPHYV----SAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFG 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 PVTGIPVG-MFYPAPPMERVVSCRMAPAAGGA-WTTALCDCADDCNTCCMACWCPCIPVG 76
         64
                               84
                                                                                                                                                                                                                                                                  Tracheophyta;
         VGYNLGLMKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEIL
                               25 VSHNGGIGKPANIPTGIPVNYQQTQNQWSSQLFDCMNDSENAVITLIAPCVTFGQIAEIV
                                                      NKGTTSCGSRGALYCLLGLTGLPSLYSCFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALC
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 161;
                                                                                                                                                                                                                                                                                                                                      Wood T., Yu Y., Soderlund
                                                                                                                                                                                                                                                     Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideee; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 299.5; DB 10; Length
Pred. No. 9.6e-27;
0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                  Wing R.A., Frisch D., Presting G., Wood T., Yu Y., Soder Kim H., Rambo T., Henry D., Simmons J.; "Rice Genomic Sequence."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; ACO7968; AAK2582.1; SEQUENCE 161 AA; 17230 WW; 6966EBB537413153 CRC64;
                                                                                                                                                                                                       Created)
Last sequence update)
Last annotation update)
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Last annotation update)
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                                                                                                 125 QEYRELKNRGFDMGIGWQANMDR-QSRGVTMPP 156
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01-MAR-2001 (TrEMBLrel. 16, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
HYPOTHETICAL 21.2 KDA PROTEIN.
F915.19.
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                                                                                                                                                                                                                                                                                                                                                                                                                   32.5%; Scc.
42.9%; Pred
20;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
UNKNOWN PROTEIN.
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Best Local Similarity
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Matches
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71 KHLDFGGNAACMNAGLIHIALGFIGCSWLYAFPNRSRLREHFALPEEPCRDFLVHLFCTP 130
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
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Sakano H.,
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Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysociskala V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J.M., Li J., Gonzalez A., Liu A., Liu K., Vaysberg M., Sakano H.,
Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Huyng B., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
The sequence of BAC F24J5 from Arabidopsis thaliana chromosome 1.",
Submitted (AuG-1999) to the EMBL/GenBank/DDBJ databases.
EMBL. ACO08075: AAD499821; --
SEQUENCE 174 AA, 19612 MW; E46BA0F52F9F9A71 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVPPHYVSAPGTTTA--RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                                                                                                                                                                                                                                                                                                                                                                     35 FAPPNYQQANVNLSVGRPWSTGLFDCQADQANAVLTTIVPCVTFGQIAEVMDEGEMTCPL 94
  Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.; "Arabidopsis thatlana chromosome I BAC F915 genomic sequence."; Submitted (OCT-2000) to the EMBL/GenBank/DDbJ databases. EMBL; AC022354; AAF29406.2;
                                                                                                                                                                                                                                                                                          18;
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                                                                                                                                                                                                                                  Length 190;
                                                                                                                                                                                                                                                                                          Indels
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4; E468A0F52F9F9A71 CRC64;
                                                                                                                                              21179 MW; 9708EF167B0031C0 CRC64;
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Last annotation update)
                                                                                                                                                                                                                               Score 288; DB 10;
Pred. No. 2.5e-25;
7; Mismatches 44;
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Bowman C.L., White O., aliana chromosome 1 BAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||| | | :|| | :|| ELKIRNLDPSLGWNGILAQGQGGYEREA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                  31.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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190 AA; 2
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OI-WAR-2001 (TERMELEI. 16, Created)
OI-MAR-2001 (TERMELEI. 16, Last sequence update)
OI-DEC-2001 (TERMELEI. 19, Last annotation update)
OI-DEC-2001 (TERMELEI. 19, Last annotation update)
TI4P1.19/AT2645010.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Coldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
Kamiya A., Karlin-Neumann G., Rawai J., Kim C., Lam B., Lin J.,
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.
"Full Length cDNA of gene T14P1.19/At2g45010 (GI:4895249).";
Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
BMBL; AF327424, AAG42014.1;
NON_TER 238 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 VLPETYEPP-----SDENWTTGIFGCAEDPESCRTGLFCPCVLFGRNIEAVREEIPW 100
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11 LINKQPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNK---G 67
                                                                                                                     Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                      16;
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
"Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1,
clone:P0011D01.";
                                                                                                                                                                                                                                                                                                                                                                                                                   29; Indels
                                                                                                                                                                                                                                                                                        Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AP000969; BAA88537.1; -- SEQUENCE 147 Aa; 15696 MW; 950D30EZA111508B CRC64;
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238 AA; 26581 MW; B272FAA3E46A7FB7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ESTS AU082078(C53435).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 CFYRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYRELKNR 133
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39.2%; Pred. No. 1.8e-14;
iive 17; Mismatches 29;
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 147 AA
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 PRT;
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nes 40; Conservative
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Matches
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AAG38298

AAG14720 AAG46458 AAG36901 AAG36901

AAG40344

AAG51030 AAG51029 AAG10396

AAG10395 AAG24599 AAG30353 AAG49966 AAG51031

AAG10397 AAB08524

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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                               MYPTVGYNLGLMKQPYVPPH........NMDRQSRGVTMPPYHAGMTR 163
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Copyright (c) 1993 - 2000 Compugen Ltd
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence. Arabidopsis thallana protein fragment SEQ ID NO: 45286. AAG36900 standard; Protein; 152 AA 990S-0121825. 99US-0123180. 99US-0125788. 99US-0125788. 99US-0126785. 99US-0127462. 99US-0128714. 99US-0128714. 99US-0128714. 25-FEB-2000; 2000EP-0301439 18-OCT-2000 (first entry) Arabidopsis thallana. 25 - FEB - 1999; 05 - MAR - 1999; 03 - MAR - 1999; 25 - MAR - 1999; 25 - MAR - 1999; 01 - APR - 1999; 06 - APR - 1999; EP1033405-A2 16-APR-1999; 19-APR-1999; 21-APR-1999; 06-SEP-2000 AAG36900; AAG36900

Arabidopsis thalia Pathogen response Arabidopsis thalia

AAG39510 AAG16620 AAG16619 AAG16613 AAG10515 AAG10515 AAG10514 AAG14719 AAG14719

152 160 173 173 191 190 190 190

447.0 446.1 443.8 443.8 339.4 331.4 331.4 30.5

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<u></u>	26 - UGL 1999; 27 - UGL 1999; 27 - UGL 1999; 28 - UGL 1999; 02 - AGG 1999; 03 - AGG 1999; 04 - AGG 1999; 05 - AGG 1999; 06 - AGG 1999; 06 - AGG 1999; 06 - AGG 1999; 07 - AGG 1999; 11 - AGG 1999;	,	, <u>ത്</u> യത്ത്യയയെയെയെയെയ
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99US-0141842
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99US-0143624
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                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                       16 YVPPHYVSAPCTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGSRG 75
                                                                                                                                                                                                                                                                                                                   40; Indels 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG39510 standard; Protein; 152 AA
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
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52.0%; Pred. No. 2.5e-37;
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48.5%; Pred. No. 5.7e-35;
ive 27; Mismatches 41; Indels 17;
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                                                                                                                                                                                                                                                                                                                          124 CQEYRELK-NRGFDMGIGWQANMDRQSR----GVTMPPYHAGMTR 163
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Matches 80; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 43.8%; Score 403; DB 21; Length 151;
Best Local Similarity 48.4%; Pred. No. 5.5e-35;
Matches 75; Conservative 21; Mismatches 47; Indels 12; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QPYVPPHYVSAPGTTTARWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
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             990S-0159295.
990S-0159339.
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990S-0159634.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                            39.4%; Score 363; DB 21; Length 133; 52.3%; Pred. No. 8.5e-31; ive 24; Mismatches 30; Indels
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18-JUN-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 RGALYCLLGLTGLFSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54; Indels 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 8869.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELKNRGFDMGIGW-----QANMDRQSRGVTMPPYHAGMTR 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG10514 standard; Protein; 194 AA
990S - 0159293 . 990S - 0159294 . 990S - 0159294 . 990S - 0159329 . 990S - 0159330 . 990S - 0159331 . 990S - 0150981 . 990S - 0151920 . 990S - 0151922 .
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990S-0125788.
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13 - OCT - 1999;

13 - OCT - 1999;

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23-MAR-1999;
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Re in July 1999 9908-014509.

Re in July 1998 9908-014509
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74 RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
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herbicide resistance;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.4%; Score 289; DB 21; 38.1%; Pred. No. 9.9e-23;
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                     9908 - 0159293
9908 - 0159294
9908 - 0159295
9908 - 0159329
9908 - 0159330
9908 - 0159331
9908 - 0159637
9908 - 0159584
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9908 - 0160768
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25-0CT-1999;
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  \frac{1}{2}
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                                                                                                                       This is the amino acid sequence of LSD1-interacting protein K of Arabidopsis thaliana. LSD1 interacting genes (see AAV66755-67) were isolated from a yeast gene expression library constructed in plasmid pdG4-5 using RNA from Arabidopsis leaves infected with Pseudomonas syringae. A two-hybrid system was used with LSD1 short and long open reading frames (see AAV66750-51) as bait. LSD1 (see AAW72366-67) is a novel polypeptide that regulates the initial response of plants to pathogens and the subsequent spread of plant cell death engendered by infection. Since the inactivation of LSD1 by mutation leads to enhanced disease resistance, LSD1 partner proteins represent novel targets for engineering plants with enhanced resistance to pathogens. Thus, the invention includes all proteins (see AAW72384-96) that interact with the cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                                     74 RGALYCLLGLTGLPSLYSCF----YRSKMRGQYDLEEAPCVDCLVHVFCEPCALCQEYR 128
                                                                                                                                                                                                                                                                                                                                                                                           : ||:| | : ||||| | | | | | :||: ||:|||||:|| :|| :|| 33 fappnyqqanvnlsvgrpwstglfdcqadqanavlttivpcvtfgqiaevmdegemtcpl 92
                                                                                                                                                                                                                                                                                                                                                       44; Indels 18; Gaps
                                                                                                                                                                                                                                                                                                                                                                              16 YVPPHYVSAPGITIA--RWSTGLCHCFDDPANCLVTSVCPCITFGQISEILNKGTTSCGS 73
                                                      New isolated Arabidopsis genes - useful for producing transgenic plants which show resistance to cell death caused by pathogens or herbicides.
                                                                                                                                                                                                                                                                                                                                31.3%; Score 288; DB 19; Length 188; 39.9%; Pred. No. 1.2e-22; Live 27; Mismatches 44; Indels 18
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 Richberg MH;
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 Epple PM,
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                                                                                                  Claim 46; Page 63; 88pp; English.
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 Dangl JL, Dietrich RA,
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                      WPI; 1998-531501/45.
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PR 19-JUL-1999; 990S 0144325.

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PR 19-JUL-1999; 990S 0144331.

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PR 19-JUL-1999; 990S 0144331.

PR 20-JUL-1999; 990S 0144331.

PR 20-JUL-1999; 990S 0144333.

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PR 21-JUL-1999; 990S 0144334.

PR 22-JUL-1999; 990S 0144334.

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PR 22-JUL-1999; 990S 0144314.

PR 22-JUL-1999; 990S 0145214.

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PR 22-JUL-1999; 990S 0145218.

PR 22-JUL-1999; 990S 0145218.

PR 22-JUL-1999; 990S 0145218.

PR 22-JUL-1999; 990S 0145219.

PR 22-JUL-1999; 990S 0155219.

PR 23-JUL-1999; 990S 0155219.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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es 37; Indels 45;
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llarity 37.4%; Pred. No. 7.8e
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PR 19-JUL-1999; 99US-0144332.

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PR 23-JUL-1999; 99US-01508.

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Best Local Similarity 45.5%; Pred. No. 5.2e-17;
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13-AUG-1999;
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20-AUG-1999;
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51.9%; Pred. No. 1.7e-16;
iive 11; Mismatches 23;
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99US-0162142.
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61 qnqggvamgapafqggmtr 79
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06-APR-1999;
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05-OCT-1999;
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                                                                                                                                                                                                                                                                                               45 NCLVTSVCPCITFGQISEILNKGT-----TSC------GSRGALYCLLGLTG- 85
                                                                                                                                                                                                                                                                           27; Indels 22;
                                                                                                                                                                                                                                                          Length 133;
                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana protein fragment SEQ ID NO: 58450.
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15; Mismatches 27;
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99US-0159329.
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99US-0159637.
99US-0159638.
99US-0159638.
99US-0160740.
99US-0160814.
99US-0160814.
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40.7%;
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Best Local Similarity 40.70,
These 44; Conservative
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05-MAR-1999;
03-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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21-APR-1999;
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